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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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1789
1 MLQKPKSVKLRALRSPRKEG.....SRIYKPQTRLKRKQPVRKRQ 338
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458
1019
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                                            P56201 oryctolagus
P2323 xenopus lae
P12502 sinian immu
P12503 human immun
P17757 human immun
P01029 mus musculu
P18042 human immun
P42487 african swi
O00273 homo sapien
O74454 schizosacch
O95613 homo sapien
O94644 homo sapien
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45	44	43	42	41	40	39	38	37	36	35	34
83.5	83.5	84	84	84	84.5	84.5	84.5	85.5	85.5	85.5	86
4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.8	4.8	4.8	4.8
308	239	526	219	217	3859	1056	373	1744	736	331	1027
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YDM7_SCHPO	FS27_MOUSE	G6PD_CERCA	CIDB_MOUSE	CIDA_MOUSE	RPOA_LELV	POL_SIVM1	CONS_ARATH	CO4_HUMAN	XMS1_DROME	DFFA_MOUSE	KINN_MOUSE
P87138 schizosacch	P56198 mus musculu	P41571 ceratitis c	070303 mus musculu	070302 mus musculu	Q04561 lelystad vi	P05896 simian immu	Q39057 arabidopsis	P01028 homo sapien	Q9u3v8 drosophila	mus	£33175 mus musculu

ALIGNMENTS

RESULT DEFB_H AC O DT 11 DT 1 DT 1 DT 1 CO DE (CO DE (DEFB_HUMAN ID DFFB_HUMAN STANDARD; PRT; 338 AA. AC 076075; 060521; 09BYI4; 09BYI5; Q9BYI6; DT 16-0CT-2001 (Rel. 40, Created) DT 15-UN-2002 (Rel. 41, Last sequence update) DT 15-UN-2002 (Rel. 41, Last annotation update) DE DNA fragmentation factor 40 kDa subunit (PC 3) (DFF-40) DE (Caspase-activated deoxyribonuclesse) (Caspase-activated DNase) C(Caspase-activated nuclesse) (CASPASE-activated DNase) GN DFFB OR DFF2 OR DFF40 OR CAD.
22222	Homo sapiens (Human). Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. MCBI_TaxID=9606;
2	[1] SEQUENCE FROM N.A. (ISOFORM ALPHA). MEDLINE-98337937; PubMed-9671700;
RA	Liu X., Li P., Widlak P., Zou H., Luo X., Garrard W.T., Wang X.; "The 40-kDa subunit of DNA fragmentation factor induces DNA
	during apoptosi
	SEQUENCE FROM N.A. (ISOFORM ALPHA).
R	MEDLINE-99336121; PUDMcG=9689044; Mukae N., Enari M., Sakahira H., Fukuda Y., Inazawa J., Toh H., Nacata S.:
3 2	"Molecular cloning and characterization of human caspase-activated DNase.":
2	Proc. Natl. Acad. Sci. U.S.A. 95:9123-9128(1998).
70 7	SEQUENCE FROM N.A. (ISOFORM ALPHA).
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R R	Curr. Biol. 8:537-540(1998).
88	SEQUENCE FROM N.A. (ISOFORMS BETA; GAMMA AND DELTA). TISSUE-Fetal brain;
RI.	Nakagawara A., Takahashi M., Takada N., Kawamoto T.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
R	
2 3	MEDLINE=20289753; PubMed=10830907;
R R	Judson H., van Roy N., Strain L., Vandesompele J., Van Gele M.,
RI :	
7 7	factor 40 (caspase-activated nuclease),
2.2	Genet. 106:406-413(2000).
88	-i- FUNCTION: Nuclease that induces DNA iragmentation and chromatin condensation during apoptosis. Degrades naked DNA and induces
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HSSP; (
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VARSPLIC
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DOMAIN
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L; AB013918; BAA32250.1; --
L; AF039210; AAC39709.1; --
L; AB028911; BAB40447.1; --
L; AB028912; BAB40448.1; --
L; AB028913; BAB40449.1; --
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ALTERNATIVE PRODUCTS: 4 isoforms; Alpha (shown here), Beta, and Delta; are produced by alternative splicing.
SIMILARITY: CONTAINS 1 CIDE-N DOMAIN.
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       301
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000273; 1:
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LVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ
                            LVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ
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                                                                                                                        INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK 300
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IPR003508; CAD.
-^17. CIDE-N; 1.
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GVLLCGPG (IN ISOFORM BETA).
YVSDIRFFLSAFHEPQVGLIQAAQQLLCDEQAPQRQ ->
VGVRARTKTRDTSSLSPGDCQALGNGGRCGQRLFL (IN
ISOFORM GAMMA).
MISSING (IN ISOFORM GAMMA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1789; DB 1;
Pred. No. 5.3e-147;
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0B0F3F8D91209389 CRC64;
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YVSDIRRFLSAFHEPQVGLIQAA ->
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DFFB_MOUSE
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Best Local :
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"Role of ICAD cleavage in CAD activation and DNA degradation.";
Nature 391:96-99(1998).
-I- FUNCTION: Nuclease that induces DNA fragmentation and chrom-
condensation during apoptosis. Degrades naked DNA and induc-
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DFFB OR CAD.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata; Metazoa; Rodentia;
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                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1196287; Dffb.
InterPro; IPR003508; CAD.
Pfam; PF02017; CIDE-N; 1.
SMART; SM00266; CAD; 1.
                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB009377; BAA24977.1; HSSP; 000273; 11BX.
                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institute modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98082976; PubMed-9422513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA fragmentation factor 40 kDa subunit (EC 3.-...) (DFF-40) (Caspase-activated deoxyribonuclease) (Caspase-activated DNase) (CAD). DFFB OR CAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 391:43-50(1998). 6/
                                                                                                                                                                                                                                                                                                                                                                                                                                send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic and nuclear SIMILARITY: CONTAINS 1 CIDE-N DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apoptotic morphology.
ENZYME REGULATION: Inhibited by DFFA (DFF45).
SUBUNIT: HETERODIMER OF A 45 kDa AND A 40 kDa
184
                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                        124
                                                                                                                                                                                                                                  261;
                                                                                                                 64
                                                                                                                                                                          4
                                                                                                                                                                                       Similarity
              EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS
                                                                      DLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGA
                                                                                                                              PSVPDNAELVLLTLGQAWGGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLA
                                                                                                                                                                     VLRQPKCVKLRALHSACKFGVAARSCQELLRKGCVRFQLPMPGSRLCLYEDGTEVTDDCF
AAQEEYLRVLGSMCQKLKSVQYNGSYFDRGAEASSRLCTPEGWFSCQGPFDLESCLSKHS
                                                       DLLHHVSQNITAETREQDPSWFEGLESRFRNKSGYLRYSCESRIRGYLREVSAYTSMVDE
                                                                                                               PGLPNDAELLLLTAGETWHGYVSDITRFLSVFNEPHAGVIQAARQLLSDEQAPLRQKLLA
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
tation factor 40 kDa subunit (EC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                              79.28;
77.28;
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                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                               Score 1416; DB 1;
Pred. No. 8.2e-115;
37; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                        E854B413EA139DE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Okawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                during apoptosis, and
                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and chromatin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last anotation update)
DNA fragmentation factor 40 kDa subunit (EC 3.----)
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003508; CAD. Pfam; PF02017; CIDE-N; 1. SMART; SM00266; CAD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuronal cultures.";
7. Meurosci. 21:4678-4690(2001).
7. Meurosci. 21:4678-4690 (2001).
7. FUNCTION: Nuclease that induces DNA fragmentation and chromat.
7. FUNCTION: Author annotosis. Degrades naked DNA and induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE-21319171; PubMed-11425895;
Cao G., Pei W., Lan J., Stetler R.A., Luo Y., Nagayama T.,
Graham S.H., Yin X.M., Simon R.P., Chen J.;
"Caspase-activated DNase/DNA fragmentation factor 40 mediates
apoptotic DNA fragmentation in transient cerebral ischemia and in
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- ENVYME REGULATION. Inhibited by DEFA (DFF45).
-!- SUBGUNIT: HETERODIMER OF A 45 KDA AND A 40 KDA SUBGUNIT.
-!- SUBCELLGLAR LOCATION: Cytoplasmic and nuclear (By similarity).
-!- SIMILARITY: CONTAINS 1 CIDE N DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rai
                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Caspase-activated
                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apoptotic morphology.
ENZYME REGULATION: In:
SUBUNIT: HETERODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR CAD.
    124
                      121 DLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK
                                                                                                                                                                                                                                                       257;
                                                                                                                                                                                                         1 MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          norvegicus (Rat).
                                                                                                                                                                                                                                                                           Similarity
DLLHHVSQNITAETREQDPSWFEGLESRFRNKSGYLRYSCESRIRGYLREVSAYISMVDA
                                                                                                                                                                 VLPQPKCVKLRALHSSCKFGVAARSCQELLRKGCIRFQLPVPGSRLCMYEDGTEVTDDCF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVHIACHKKTTHKLECDRSRIYRPQTGSRRKQPARKKR 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INPYGNRESRILFSTWNLDHIIEKKRTVVPTLAEAI--QDGREVNWEYFYSLLFTAENLK
                                                                                PSIPNDSELLLLTAGETWHGYYSDITRLLSVFNEPHAGVIQAARQLLSDEQAPLRQKLLA 123
                                                                                                                        PSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLA 120
                                                                                                                                                                                                                                                                                                                                                          Nuclease; Nuclear protein; Apoptosis. 7 83 CIDE-N.
                                                                                                                                                                                                                                                                                                                                        349 AA;
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deoxyribonuclease) (Caspase-activated DNase) (CAD).
                                                                                                                                                                                                                                                                                                                                      40096 MW;
                                                                                                                                                                                                                                                                         77.8%;
                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                 Score 1392; DB 1;
Pred. No. 9.9e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                      F125972A110FE398 CRC64;
                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                                                          Length 349;
                                                                                                                                                                                                                                                  Indels
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01-FEB-1996
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -I- FUNCTION: INTEGRAL COMPONENT OF THE FILAMENTOUS MATRIX OF THE CENTROSOME INVOLVED IN THE INITIAL ESTABLISHMENT OF ORGANIZED MICROTUBBLIE ARRAYS IN BOTH MITOSIS AND MEIOSIS:
-I- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN KIDNEY, THYMUS AND LIVER, LOW LEVELS IN BRAIN, MUSCLE, LUNG AND HEART.
-I- DOMALN: COMPOSED OF A COILED-COIL CENTRAL REGION FLANKED BY NON-HELICAL N- AND C-TERMINALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCNT_MOUSE
P48725;
                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microtubule organization.";
Cell 76:639-650(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doxsey S.J., Stein P., Evans L., Calarco P.D., Kirschner M.; "Pericentrin, a highly conserved centrosome protein involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - I - SIMILARITY: STRONG, TO HUMAN KENDRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94170365; PubMed=8124707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pericentrin
                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                        MGI:102722; Pcnt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302
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108 CDEQAPQRQRLL------ADLLHNVSQNIAA-----ETRAEDPPWFEGLESRFQSKSG 154
                                                                                                                142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 AAREEYLRVLSSMCHKLKSVQYNGSYFDRGAEASSRLCTPEGWFSCQGPFDLESCLSKHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS
                                              198 AAELKEKLRSEMEKNAQ-TIETLKQDWESERELCLENLRQELSLKHQSEMEGLQSQFQKE 256
                                                                                                                                            2 LOKPKSYKLRALRSPRKFGVAGRSCQEVL----RKGC----LRFQLPERGSRLCLY--ED
                                                                                                                                                                                                                                                                                                             CO11;
                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK 300
                                                                              GTELTEDYFPSVPDNAELVLLTLGQAWQG----YVSDIRRFLSAFHEPQVGLIQAAQQLL 107
                                                                                                              LQKEKETALTELREM----LNGRRAQELALLQSRQQCELELLREQHAREKEEMALRSGQE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVHIACHKKTTHKLQCDRSRIYRPQTGSRRKQPPRKQ 338
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                                                                                                                                                                                                                                         383 3
1920 AA;
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(Rel. 33,
(Rel. 39,
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                           110
                                                                                                                                                                                                                                                                                                         Microtubules.
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                                                                                                                                                                                                                                                                                            1600
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23.9%;
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Rodentia;
                                                                                                                                                                                                                                           218337 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence up
Last annotation
                                                                                                                                                                             45;
                                                                                                                                                                                         Score 108.5;
Pred. No. 0.
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POLY-PRO.
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                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                           CF1D0ADEC5B73309 CRC64;
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                                                                                                                                                                                            .48;
                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                          Length 1920;
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RESULT 5
VIME_MOUSE
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P20152; 0087/
01-FEB-1991
01-MAY-1992
15-JUN-2002
                 Ando S., Tokui T., Yamauchi T., Sugiura H., Tanabe K., "Evidence that Ser-82 is a unique phosphorylation site for Ca2(+)-calmodulin-dependent protein kinase II."; Biochem. Biophys. Res. Commun. 175:955-962(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Spleen;
STRAIN-C57BL/6; TISSUE-Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-89306653;
                                                                                                                                                                                                                                                                                                                  myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Capetanaki Y., Kuisk I., Rothblum K., Starne Mouse vimentin: structural relationship to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood L., Theriault N., Vogeli G.; "Vimentin cDNA clones covering the protein are found in an EHS tumor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                using preparative two-dimensional Electrophoresis 15:735-745(1994).
                                                                                                                                                            Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.; "Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
                                                                                                                                                                                                                                          TISSUE-Fibroblast;
                                                                                                                                                                                                                                                           SEQUENCE OF 71-90.
                                                                                                                                                                                                                                                                                             "Transcriptional regulation myeloid leukemia MI cells."; Gene 166:281-286(1995).
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96125204;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90265604; PubMed=2140597; Capetanaki Y., Kuisk I., Rothblum
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                                                                                           MEDLINE-91222208; PubMed-1850997;
                                                                                                              PHOSPHORYLATION OF
                                                                                                                                                                                                                                                                                                                                                     Nakamura N., Shida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
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Bloemendal H., Quax W., Quax Jeuken Y., Dodemont H., Ramaekers Dunia I., Benedetti L.;
"Organization and expression of the vimentin gene.";
Mol. Biol. Rep. 9:115-118(1983).
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                                                                          DB 1; Length 448;
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                                                                 . 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986
21-JUL-1986
15-JUN-2002
EMBL; K00927; AAA37104.1;
EMBL; K00921; AAA37104.1;
EMBL; K00922; AAA37104.1;
EMBL; K00922; AAA37104.1;
EMBL; K00924; AAA37104.1;
                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE-83221633; PubMed-6304716;
Quax-Jeuken Y.E.F.M., Quax W.J., Bloemendal H.;
"Primary and secondary structure of hamster vimentin predicted from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                ++
                                                                                                                                                                                                                                                                                                                                              the nucleotide sequence.";

Proc. Natl. Acad. Sci. U.S.A. 80:3548-3552(1983).

1- FUNCTION: Vimentins are class-III intermediate filaments found various non-epithelial cells, especially mesenchymal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The structure of the vimentin gene."; Cell 35:215-223(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quax W.J., Egb
Bloemendal H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-84026520; PubMed-6194898;
Quax W.J., Egberts W.V., Hendriks W., Quax-Jeuken Y.E.F.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesocricetus.
NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vimentin
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P02544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           SUBUNIT: HOMOPOLYMER.

PTM: ONE OF THE MOST PROMINENT PHOSPHOPROTEINS IN VARIOUS CELLS MESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DURING CELL DIVISION, AT WHICH TIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY
                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC
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(Rel. 01, Last sequence update)
(Rel. 41, Last annotation update)
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CONFLICT
STRAIN-Fischer;
MEDLINE-92171936; PubMed-1540169;
Bussemakers M.J.G., Verhaegh G.W.
                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                    01-JUL-1993
01-JUL-1993
15-JUN-2002
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EMBL; K00926; AAA37104.1;
PIR; A02959; VEHY
                                           SEQUENCE FROM N.A.
                                                                                                             Rattus norvegicus
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Pfam; PF00038; filament;
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oa; Chordata;
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COIL 1B.
LINKER 12.
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Pred. No.
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7; Mismatches
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PHOSPHORYLATION
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                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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7AC417008CBD4776 CRC64;
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PIR; JQ1389; JQ1389.
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InterPro; IPR001664; IF. Pfam; PF00038; filament; PR0017E; PS00226; IF; 1.
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"Differential expression of vimentin in rat prostatic tumors.";
""""" #10phys. Res. Commun. 182:1254-1259(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (some send an email to license@isb-sib.ch).
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PTM: ONE OF THE MOST PROMINENT PHOSPHOPROTEINS IN VARIOUS CELLS MESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DIVISION, AT WHICH TIME VIMENTIN PARTICLES IN PROPERTY.
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RESULT 9
VIME_HUMAN STANDARD; PRT; 465 AA.
ID VIME_HUMAN STANDARD; PRT; 465 AA.
AC P08670; 015867; 09NTM3; 015869; Q15868;
DT 01-JAN-1988 (Rel. 27, Last sequence update)
DT 01-0CT-1993 (Rel. 41, Last annotation update)
                                                  TISSUE-Osteosarcoma;

MEDLINE-90215314; PubMed-2323579;

Gupta A.K., Aubin J.E., Waye M.M.Y.;

"Isolation of a human vinentin cDNA with a long 3'-noncoding region from a human osteosarcoma cell line (MG-63).";

Gene 86:303-304(1990).
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MEDLINE-8303836; PubMed-2472876;
Sommers C.L., Walker-Jones D., Heckford S.E., Worland P.,
Valverius E., Clark R., McCormick F., Stampfer M., Abularach S.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                   transcription in ti
Gene 62:7-16(1988).
                                                                                                                                                                                                                                                                                                                            Perreau J., Lilienbaum A., Vasseur M., Paulin D.;
"Nucleotide sequence of the human vimentin gene and regulation of its transcription in tissues and cultured cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Vimentin rather than keratin expression in some hormone-independent breast cancer cell lines and in oncogene-transformed mammary
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SEQUENCE OF 16-24 AND 54-69
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Nucleic Acids Res. 18:6692-6692(1990)
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PHCI-2DPAGE; P08670; ......
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MEDLINE-97295304; PubMed-9150946;
Rasmussen R.K., J1 H., Eddes J.S., Moritz R.L., Reid G.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VATIOUS NON-EPITHELIAL CELLS, especially mesenchymal cells.
SUBUNIT: HOMOPOLYMER.
TISSUE SPECIFICITY: Highly expressed in fibroblasts, some expression in T and B lymphocytes, and little or no expression is Burkitt's lymphoma cell lines. Expressed in many hormone-independent mammary carcinoma cell lines.
PTM: ONE OF THE MOST PROMINENT PHOSPHOPATIENS IN VARIOUS CELLS MESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DURING CELL
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Hess J.F., Casselman J.T., FitzGerald P.G.;
"Nucleotide sequence of the bovine vimentin-encoding cDNA.";
Gene 140:257-259(1994).
-I- FUNCTION: Vimentins are class-III intermediate filaments found i various non-epithelial cells, especially mesenchymal cells.
-I- SUBUNIT: HOMOPOLYMER.
-I- SUBUNIT: HOMOPOLYMER.
-I- PTM: ONE OF THE MOST PROMINENT PHOSPHOPROTEINS IN VARIOUS CELLS MESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DURING CELL DIVISION, AT WHICH TIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY
                        entities requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
                                                   use by non-profit institutions as long modified and this statement is not removed
                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKTVETRDGQVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGPFDMDSCLSRHSINPYSNRESRIL----FST----WNLDHI----IEKKRTIIPTL
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                                                                              Bioinformatics Institute.
AAA53661.1;
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Last annotation update)
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S -> C (IN REF. 7).
N -> K (IN REF. 7).
F -> L (IN REF. 4, 5, 7 AN 658EC88732865FF1 CRC64;
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Best Local S
Matches 64
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INIT_MET
DOMAIN
DOMAIN
       Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain w code for large proteins in vitro."; DNA Res. 4:141-150(1997).
                                                                                                                                                                                   015068;
15-JUL-1999 (Rel. 38,
15-JUL-1999 (Rel. 38,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
- I -
                                                                                                                                 Eukaryota;
                                                                                                                                                             transforming sequence-like
                                                                                                                                                              15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
Guanine nucleotide exchange factor DBS (DBL's
transforming sequence-like protein) (Fragment)
                                                                     MEDLINE=97349984; PubMed=9205841;
                                                                                         SEQUENCE
                                                                                                               NCBI_TaxID=9606;
                                                                                                                         Mammalia;
                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                       MCF2L OR KIAA0362
                                                                                                                                                                                                                             DBS_HUMAN
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TE; PS00226; IF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
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                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                               IKTVETRDGQVIN 455
                                                                                                                                                                                                                                                                                                                                     VEAIKEQDGREVD
                                                                                                                                                                                                                                                                                                                        KMALDIEIATYRKLL---EGEESRISLPLPNFSSLNLRETNLDSLPLVDTHSKRTL---
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                                                                                                                                                                                                                                                                                                                                                                                   YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AFLKKLHDAEIQELQAQIQEQHVQIDMDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
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                                                                                                                       Eutheria;
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                                                                                                                                  Metazoa;
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GUANINE
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                                                                                                                       Chordata;
Primates;
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NUCLEOTIDE
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Pred. No.
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LINKER 1.
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                                                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119E126778BF5801 CRC64;
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EXCHANGE
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0.92;
FACTOR THAT POTENTIALLY
                                                                                                                      Hominidae;
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                                                                                                                                                                          sister)
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                                                                                                                                                                          (MCF2
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                                                                                                                                                                                                                                                                                                                                                                -DLLNV
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Best Local S
Matches 83
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Pfam; PF00435; Spectrin; 1.
Pfam; PF00621; RhOGEF; 1.
SMART; SM00233; PH; 1.
SMART; SM00235; RhOGEF; 1.
SMART; SM00516; SEC14; 1.
SMART; SM00150; SPEC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50191; CRAL_TRIO; 1.
PROSITE; PS00741; DH_1; 1.
PROSITE; PS50010; DH_2; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINKS PATHWAYS THAT SIGNAL THROUGH RAC1, RHOA AND CDC42 CATALYZES GUANINE NUCLEOTIDE EXCHANGE ON RHOA AND CDC42 AND INTERACTS SPECIFICALLY WITH THE GTP-BOUND FORM OF RAC1, SUGGESTING THAT IT FUNCTIONS AS AN EFFECTOR OF RAC1. MAY ALSO PARTICIPATE IN AXONAL TRANSPORT IN THE BRAIN. BECOMES ACTIVATED AND HIGHLY TUMORIGENIC BY TRUNCATION OF THE N-TERMINUS (BY SIMILARITY).

1- SIMILARITY: CONTAINS 1 DEL-HOMOLOGY (DH) DOMAIN.

1- SIMILARITY: CONTAINS 1 CRAL-TRIO DOMAIN.
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                                                                                                                                                                     153
                                                                                                                                                                                                                                                                                                             445 RPKCQELRHLCDQFSAEIARRRGLLSKSLELHRRLETSMKWCDEGIYLLASQPVDKCQSQ 504
                                                                                                                                                                                                505 DGAEAALQEIEKFLETGAENKIQELNAIYKEYESILNQDLMEHVRKVFQKQASMEEVFHR 564
                                                                                                                                                                                                                         95 PQVGL--IQAAQQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSK 152
                                                                                                                                                                                                                                                                                 51 DGTELT-EDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFL-----SAFHE 94
                                                                                                                                                                                                                                                                                                                                                                       83;
                                                                                                                                                                                                                                                                                                                                           4 KPKSVKLRAL-----RSPRKFGVAGRSCQ-----EVLRKGCLR--FQLPERGSRLCLYE 50
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                          RELENYTDCPELYGRCFLERMEDFQIYEKYCQNKPRSESLWRQCSDCPFFQE------
                                                     ---KKRTIIPTLV-----EAIKEQDGREVDWEYFYGLLFTSENLKLVHIV 305
                                                                                 ----ELLCYLEGYAA-----EMDNPLMAHLLSTGLHNKKDVLFG--NMEEIYHFHNRIFL
                                                                                                                                         GGALRRGPYRRAKSEMSESRQGRGSAGEE--EESLAILRRHVMSELLDTER---AYVE--
                                                                                                                                                                  SGYLRYSCESRIRSYLREVSSYPSTYGAEAQEEFLRYLGS--MCQRLRSMQYNGSYFDRG 210
CHKKTTHKLNCDPSRIYKPQTRLKRKQPVRK 336
                                                                                                           AKGGSRLCTPEGWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIE-----
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IPR001331; GDS_CDC24.
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                                                                                                                                                                                                                                                                                                                                                                                                                            1108 AA;
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 releasing factor; Proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                 5.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                              123983 MW;
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                                                                                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                                                                                                   Score 94.5;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DH.
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POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PH.
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                                                                                                                                                                                                                                                                                                                                                                                                Length 1108;
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Best Local S
Matches 33
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FS27_HUMAN RESULT 12 Q96AQ7: EMBL; BC016851; AAH16851.1; -. InterPro; IPR003508; CAD. Pfam; PF02017; CIDE-N; 1. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID-9606; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Fat-specific protein FSP27 homolog. FSP27. TISSUE-Colon; SEQUENCE FROM N.A. Homo sapiens (Human) send an email to license@isb-sib.ch). 765 CORKLDHKLSLD-SYLLKPVQRITKYQLLLK 794 STANDARD; 118 C 26754 MW; CIDE-N. ; 5CF774929E821DA5 CRC64; PRT; 238 AA There are no restrictions ng as its content is in

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POL_SIVIT 13
POL_SIVIT 13
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PO5897;
Ol:NOV-1988 (Rel. 09, Created)
Ol:NOV-1988 (Rel. 09, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
POL polyprotein [Contains: Protease (Retropepsin) (EC 3.4.23.-);
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
SEQUENCE FROM N.A.

MEDLINE-07287229; PubMed=3497350;

Franchini G., Gallo R.C., Guo H.-G., Gurgo C., Callatti E.,

Fargnoli K., Hall L., Wong-Staal F., Reitz M.S. Jr.;

Fargnoli K., Hall L., Wong-Staal F., Reitz M.S. Jr.;

"Sequence of simian immunodeficiency virus and its relations
the human immunodeficiency viruses.";

Nature 328:539-543(1987).

"I- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'--
                                                                                                                                                                                                                                              Simian immunodeficiency virus (K6W isolate) (SIV-MAC).
Viruses; Rettroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11/35;
                                                                                      relationship
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33; Similarity 238 AA;

Conservative

16; Mismatches

Score 92.5; DB 1; Length 238; Pred. No. 0.78; 6; Mismatches 41; Indels

9 Caps

y 33.3%;

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BAC2_HUMAN S
ID BAC2_HUMAN S
AC Q9BYV9; Q9NTS5;
DT 15-JUN-2002 (Re)
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HIV; M15897; POLS
MEROPS; A02.002;
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PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE: PS50175; ASP_PROT_RETROV; 1.
AIDS; Polyprotein; Hydrolase; Aspartyl protease; Er
AIDS; Polyprotein; Hydrolase; Aspartyl protease; Er
Nuclease; Transferase; RNA-directed DNA polymerase.
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InterPro; IPR000477; RV
InterPro; IPR001584; Rv
InterPro; IPR001587; rnaseH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001995; Aspprotease_rtrv.
InterPro; IPR001969; Aspprotease_site.
InterPro; IPR001037; Integrase_C.
InterPro; IPR003308; Integrase_Zn.
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PF02022; Integra
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1054
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Query Match

5.18;

Score

91.5;

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Length

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Nuclear protein; A
DOMAIN 37
DOMAIN 162
DNA_BIND 651
DOMAIN 674
VARSPLIC 416
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EMBL; AJ271878;
EMBL; AL121787;
HSSP; P05412; 1F
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entities requires a license agreement (S)
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                   Genew;
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-i- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS AS REPRESSOR OF ACTIVATOR. BINDS TO MAF RECOGNITION ELEMENTS (MARE). PLAY IMPORTANT ROLES IN COORDINATING TRANSCRIPTION ACTIVATION AND REPRESSION BY MAFK (By similarity).
-i- SUBMNIT: Heterodimer of BACH2 and Maf-related transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).

Melo J.V., Vieira S.D., Deininger M.W.N.;
"BACH2 expression in leukaemic cells.";
Submitted (FEB-2000) to the EMBL/GenBank/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and expression of human BACH2 mapped to chromosome 6q15." Oncogene 19:3739-3749(2000).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                       Transcription
                                                                                                                 PROSITE; PS50097; BTB; 1.
PROSITE; PS00036; BZIP_BASIC;
                                                                                                                                                                    Pfam; PF00170; bZIP; Pfam; PF00651; BTB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki S., Ito E., Toki T., Maekawa
Muto A., Nagai H., Kinoshita T., Yar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE=20404861; PubMed=10949928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
Transcription regulate
                                                                                                                                                                                             InterPro; IPR000210; InterPro; IPR004827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tromans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-612 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           produced by alternative splicing.
TISSUE SPECIFICITY: B-cell specific.
SIMILARITY: BELONGS TO THE BZIP FAMILY.
SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear (By similarity).
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factors (By similarity).
                                                                                                                                           SM00338; BRLZ; 1.
SM00225; BTB; 1.
                                                                                                                                                                                                                                   HGNC:14078; BACH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Human).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                       regulation;
                                                                                                                                                                                                                                                             1FOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rel. 41, Last sequence update)
Rel. 41, Last annotation update)
regulator protein BACH2 (BTB and
                                                                                                                                                                                                                                                                      AAK48898.1; -. CAC28130.1; -. CAB87587.1; -.
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                                                                                        Alternative
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666
539
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  92536
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                                                                                                                                                                                              TF_bZIP
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                                                                                                       Activator;
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                                                                                         splicing
                         LEUCINE-ZIPPER MISSING (IN RE
                                                  POLY-GLU.
BASIC MOTIF.
  4E926AC325952A93
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              (IN REF.
                          (IN REF.
                                                                                                     Repressor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kanezaki R., I
o M., Inazawa
                                                                                                                                                                                                                                                                                                                                                                                                                                          CNC
                                                                                                                                                                                                                                                                                                                                                               its content
                                                                                                                                                                                                                                                                                                                                                                              are no
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  CRC64;
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   VIME_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                        yara.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                       Zehner Z.E., Paterson B.M.;

**Characterization of the chicken vimentin gene: single copy gene producing multiple mRNAs.*;

Proc. Natl Acad. Sci. U.S.A. 80:911-915(1983).

1- FUNCTION: Vimentins are class-III intermediate filaments found in various non-epithelial cells, especially mesenchymal cells.

1- SUBUNIT: HOMOPOLYMER.

1- PIM: ONE OF THE MOST PROMINENT PHOSPHOPROTEINS IN VARIOUS CELLS OF MESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DURING CELL DIVISION, AT WHICH TIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY TENERGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIME_CHICK STANDARD;
p09554; Q91023;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-87250401; PubMed=3036797;

Behner Z.B., Li Y., Roe B.A., Paterson B.M., Sax

Zehner Z.B., Li Y., Roe B.A., Paterson B.M., Sax

"The chicken vimentin gene. Nucleotide sequence,
and comparison to the hamster gene.";

J. Biol. Chem. 262:8112-8120(1987).
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                               MEDLINE-83195052; PubMed-6573660;
                                                                                                                                                                                                                                  EQUENCE OF 453-459 FROM N.A.
             REORGANIZED.
SIMILARITY: BELONGS TO THE INTERNEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             689 LSERNQLK 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 YKPQTRLK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543 CEFSSSPCSQGARFLATEHQEPGLMGDGMYNQVRPQIKCEQSY-----GTNSSDESGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 REVSSYPSTVGA-----EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      494 MRPNTSCPVPIKVCPRSPP----LETRIRISS----SCSS--YSYAEDGSGGSPCSLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 ACDQVSTSVHSYSGVSSLDKDLS---EPVPKGLWVGAGQSLPSSQAYSHGGLMADHLPGR 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 VDWEYFYGLLFTSENLKLVHIV------CHKK-----TTHKLNCDPSRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 --HNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSY------L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 TQGDLKTDYTPFTGNYGQPHVGQKEVSNFTMGSPLRGPGLEALCKQEGELDRRSVIFSSS 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 APTPTAPAGAACLERSRSVASPSCLRSLFSITKSVELSGLPSTSQQHFARSPACPFDKGI 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 ---ELTEDYFPSVPD-----NAELVLLTLGQAWQG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 SPRKFGVAGRSCQE----VLRKGCLR------FQLPERG-----SRLCLYEDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSCOGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LTSEQLEFIHDVRRRSKNRIAAQRCRKRKLDCIQNLECEIRKLVCEKEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FS---EADSESC-----PVQDRGQEVKL-PFPVDQITDLPRNDFQMMIKMHK-----
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                                                                                                                                                                                                                                                                                             C.M.;
regulatory elements,
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P19505; Q88140;
01-FEB-1991 (Rel. 17, Created)
101-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
POL polyprotein [Contains: Protease (Retropepsin)
Reverse transcriptase (EC 2.7.7.49); Ribonuclease
                                         Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11738;
SEQUENCE FROM N.A.
MEDLINE=90272009; PubMed=1971917;
                                                                          Simian immunodeficiency virus (PB)14/BCL-3 isolate) (sooty mangabey)
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                            345 AVEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ--------DLLNVK
441 ETRDGQVIN 449
                                               277 KEQDGREVD
                                                                                            384 MALDIEIATYRKLL----EGEESRINMPIPTFASLNLRETNIESQPIVDTHSKRTLLIKTV
                                                                                                                                         228 GPFDMDSCLSRHSINPYSNRESRI-----LFSTWNLDHIIEKKRTIIPT-----LVEAI 276
                                                                                                                                                                                                                                        168 LREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQ
                                                                                                                                                                                                                                                                                        285 KSKFADLSEAANRNNDALRQAKQEANEYRRQIQSLTCEVDALKGSNESLERQMREMEENF
                                                                                                                                                                                                                                                                                                                                           143 ------EGLESRFQSKSGYLRY----
                                                                                                                                                                                                                                                                                                                                                                                     226 FLKKLHDEETRELQAQLQEQHIQIDMDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 DIMR---LREKLQEE----MLQREEAESTLQSFRQDVDNASLAGLDLERPVESLQEEI-V 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M15850; AAA49134.1;
M15851; AAA49134.1;
V00447; CAA23726.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                  88 FLSAFHEPQVGLIQAAQ-----QLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 EVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIRR 87
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26; IF; 1.
ilament; Coiled coil; Phosphorylation.
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19.78;
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COIL 1A.
LINKER 1.
COIL 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 91;
Pred. No.
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LINKER 12.
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(EC 3.4.23.-); H (EC 3.1.26.4)].

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ACT_SITE
SEQUENCE
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InterPro; IPR001969; /
InterPro; IPR001037; I
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HIV; M31325;
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Pfam; PF02022; Integrase_Zn; 1.
PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE; PS50175; ASP_PROT_RETROV; 1.
AIDS; Polyprotein; Hydrolase; Aspartyl protease; En Nuclease; Transferase; RNA-directed DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-92368737; PubMed-1503826;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute. There by non-profit institutions as long as ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: THE PROTEASE BELONGS KNOWN AS THE RETROPEPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: CLEAVAGE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphomonoester
CATALYTIC ACTIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DETERMINED.
                            377
                                                     121
                                                                                                                                                                                                                                                                                                                                PF00552;
PF00665;
PF02022;
  159
                                                                                                                                   265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M31325; AAA47753.1;
L03298; AAA47777.1;
                                                                                                                                                             16
                                                                                                                                                                                                                                                                                                                                                                                             PF00075; rnaseH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DNA)(N)
                                                                                                                                                                                                 Similarity
SCE--
                                                    DLLHNVSQNIAAETRAEDPPW-FEGLE
                                                                                                                                                  PRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAE----LVL 71
                        ELLNSIGFSTPEEKFQKDPPFQWMGYELWPTKWKLQKIELPQRETWTVNDIQKLVGVLNW
                                                                            KVLPQGWKGSPAIFQHTMRNVLEPFRKANPDVTLIQYMDDILIASDRTDLEHDRVVLQLK
                                                                                                         LTLGQAWQG----
                                                                                                                                 PHPAGLAKRRRITVLDVGDAYFSIP------LDEEFRQYTAFTLPSV-NNAEPGKRYIY 316
                                                                                                                                                                                                                                                                                                                                                                                                               IPR001584;
                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002156;
                                                                                                                                                                                                                                        96
1022
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLSSMMPBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVITY: N deoxynucleoside
                                                                                                                                                                                                                                                                                                                                                           integrase; 1.
                                                                                                                                                                                                                                                                                                                                                rve; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retroviruses 8:1179-1187(1992).
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                                                                                                                                                                                                                                                                   170
                                                                                                                                                                                                                                      96 BY SIMILARITY
115869 MW; 16DFBEA03
                                                                                                                                                                                                5.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                          RNaseH.
RVTse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspprotease_rtrv.
Aspprotease_site.
                                                                                                                                                                                                                                                                                                                                                                                                               Rve.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Integrase_C.
Integrase_Zn.
                                                                                                     -YVSDIRRFLSAFHE--PQVGLIQAAQQLL--CDEQAPQRQRL---LA 120
-SRIRSYLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endonucleolytic
                                                                                                                                                                                     32;
                                                                                                                                                                                                Score 90.5;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIELD THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson D.C., Mullins J.I., Fultz P.N., pathogenicity of molecularly cloned
                                                                                                                                                                                                                                                                PROTEASE
                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                        16DFBEA03F289D6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATURE PROTEINS REMAIN TO BE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cleavage
                                                                                                                                                                                                6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         triphosphate -
                                                                                                                                                                                     92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g J.I.;
derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç
                                                                                                                                                                                                              Length 1022;
                                                                                                                                                                                                                                                                                           Endonuclease;
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A2;
                                                    SRFQSKSGYLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N diphosphate
                                                                                                                                                                                     63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of.
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                                                                                                                                                                                  Gaps
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207
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THE STATE OF THE 
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                                                                     SMART; SM
SMART; SM
SMART; SM
PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINKS PATHWAYS THAT SIGNAL THROUGH RACI, KHOA AND CDC42. CATALYZES GUANINE NUCLEOTIDE EXCHANGE FACTOR THAT POTENTIALLY LINKS PATHWAYS THAT SIGNAL THROUGH RACI, KHOA AND CDC42. CATALYZES GUANINE NUCLEOTIDE EXCHANGE ON RHOA AND CDC42 AND INTERRACTS SPECIFICALLY WITH THE GTP-BOUND FORM OF RACI, SUGGESTING THAT IT FUNCTIONS AS AN EFFECTOR OF RACI. MAY ALSO PARTICIPATE IN AXONAL TRANSPORT IN THE BRAIN. BECOMES ACTIVATED AND HIGHLY TUMORIGENIC BY TRUNCATION OF THE N-TERMINUS (BY SIMILARITY).

1- TISSUE SPECIFICITY: EXPRESSED AT LOW LEVELS IN SEVERAL HEMOPOIETIC CELL LINES AND IN THYMUS AND SPLEEN, AND AT HIGHER LEVELS IN OTHER TISSUES, PARTICULARLY IN BRAIN.

1- SIMILARITY: CONTAINS 1 BH3 DOMAIN.

1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.

1- SIMILARITY: CONTAINS 1 CRAL-TRIO DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DBS_MOUSE
Q64096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitehead I., Kirk H., Kay R.; "Retroviral transduction and oncogenic selection of a Dbs, a homolog of the Dbl guanine nucleotide exchange Oncogene 10:713-721(1995).
                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:103263; MCf21.
Interpro; IPR001251; CR
Interpro; IPR001331; GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         +++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCF2L OR DBS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guanine nucleotide exchange factor DBS (DBL's
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Hematopoietic;
MEDLINE=95166559; PubMed=7862449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content ified and this statement is not removed. Usage by an
                                                                                                                                             ; PF00621; RhoGEE
T; SM00233; PH; 1
T; SM00325; RhoGE
T; SM00516; SEC14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                437
                                                                                                                                                                                                                   PF00435; spectrin; 1.
PF00621; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 DRG
                                                                                               SM00326;
SM00150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S76838; AAB33461.2; -.
                    PS50191; CRAL_TRIO; PS00741; DH_1; 1. PS50010; DH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OEG
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                                                                                                                                                                                                                                                                                                                                                                         IPR001849;
IPR000219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 38, Last sequence up
(Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence-like
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                                                                                            SH3; 1.
SPEC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                       GDS_CDC24
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRAL_TRIO
                                                                                                                                                                                                                                                                                                                        Spectrin
                                                                                                                                                                                                                                                                                                                                                                         RhoGEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
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Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
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RX MEDLINE-21848401; PubMed-11859360;
RX MEDLINE-21848401; PubMed-11859360;
RA WOOd V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA McOney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Ouall M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford X., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor R., Titzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA BOZZYM K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Nocky R., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Ra Holling R., Radler H., Wambutt R., Purnelle B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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Best Local S
Matches 74
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C 014072; 090T01; 090SD0;

T 30-MAY-2000 (Rel. 39, Created)

T 30-MAY-2000 (Rel. 39, Last sequence update)

T 15-JUN-2002 (Rel. 41, Last annotation update)

E Probable cation-transporting ATPRASE CZE11.07C

E SPAC2E11.07C OR SPACUNK4.07C OR SPARYUK71.01.

Schizosaccharomyces pombe (Fission yeast).

Schizosaccharomycetales; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetes;
Schizosaccharomyces.
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Guanine-nucleotide DOMAIN 52
DOMAIN 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 CLYEDGTELT-EDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTIIPTLVEA---IKEQDGR---------EVDWEYFYGLLFTSENLK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEKK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENSSSEGNALRRGPYRRAKSEMSEPRQGRTSSTGEE--EESLAI-----LRRHVMNEL 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRFQSKSGYLRYSCESRIRSYLREV-SSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VF-----QKQESTEEMFHRRQASLKKLAAKQTRPVQPVAPRPEALTKSPSPSPGSWRSS 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLCDEQAPQRQRLLADLLH----NVSQNIAAETRAEDP--PWFEGL------E 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CQSQDGAEASFQEIEKFLETGAENKIQELNEIYKEYECILNQ------DLLEHVQK 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50002; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1149 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Mismatches
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Pred. No. 8.8;
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WW; D9100DD133BEA9E3 CRC64;
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EMBL; AL031180; CAA20137.1; ..
EMBL; AL109734; CAB52144.1; ..
EMBL; AB027853; BAA87157.1; ..
EMBL; AB027853; BAA87157.1; ..
InterPro; IPR001757; ATPase_E1-E2.
InterPro; IPR001454; Hignase/hydrlase.
Pfam; PF00122; E1-E2_ATPase; 1.
PfAm; PF00702; Hydrolase; 1.
PRINTS; PR00119; CATATPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G. Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license(sb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fission yeast cells by the use of a GPP-fusion genomic genes cells 5:169-190(2000).

CATALYTIC ACTUTY: ATP + H(2)0 = ADP + phosphate.

-I- SUBCELLULAR LOCATION: Integral membrane protein.
 SEQUENCE
                                                                                                                                                                                                         FRANSMEM
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MEDLINE=20223868; PubMed=10759889;
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 136260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N: Integral membrane protein.
TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation; Magnesium; ATP-binding. CYTOPLASMIC (POTENTIAL).
                CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                          EXTRACELLULAR (POTENTIAL).
              MAGNESIUM
                                                                                                                          CYTOPLASMIC (POTENTIAL).
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6FEE4228CA5A57EC CRC64;
                                                                                                                                                                                         ASMIC (POTENTIAL).
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Query Match Best Local Similarity

5.0%; 20.7%;

Score Pred.

90;

DB 1; 10;

Length 1211;

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RESULT 19
G6PE_RABIT
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01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
GDH/6FGL endoplasmic bifunctional protein [Includes: dehydrogenase (EC 1.1.1.47) (Hexose-6-phosphate dehydrogenase (EC 3.1.1.31) (6FGL)].
                                                                                                                     "Isolation and the complete amino acid sequence of lumenal endoplasmic reticulum glucose-6-phosphate dehydrogenase."; Proc. Natl. Acad. Sci. U.S.A. 90:5302-5306(1993).
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                    InterPro; IPR001282; G6PD.
InterPro; IPR000457; Glucosamine_iso.
                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus
                                                                                                                                                                                                                                                                                                                                MEDLINE-93281746;
                                                                                                                                                                                                                                                                                                                                             STRAIN-New
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G6PE_RABIT
                                                            CAUTION: THE SEQUENCE IN REF.1 SEEMS TRANSPOSITION OF A SECTION THAT WAS PWHICH IS NOW TRANSPOSED TO POSITION 5
                                                                                               SIMILARITY: IN THE C-TERMINAL SECTION;
GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE;
PHOSPHOGLUCONOLACTONASE SUBFAMILY.
                                                                                                                                                       Phospho-D-gluconate.

Phospho-D-gluconate.

COFACTOR: CAN USE BOTH NAD OR NADP.

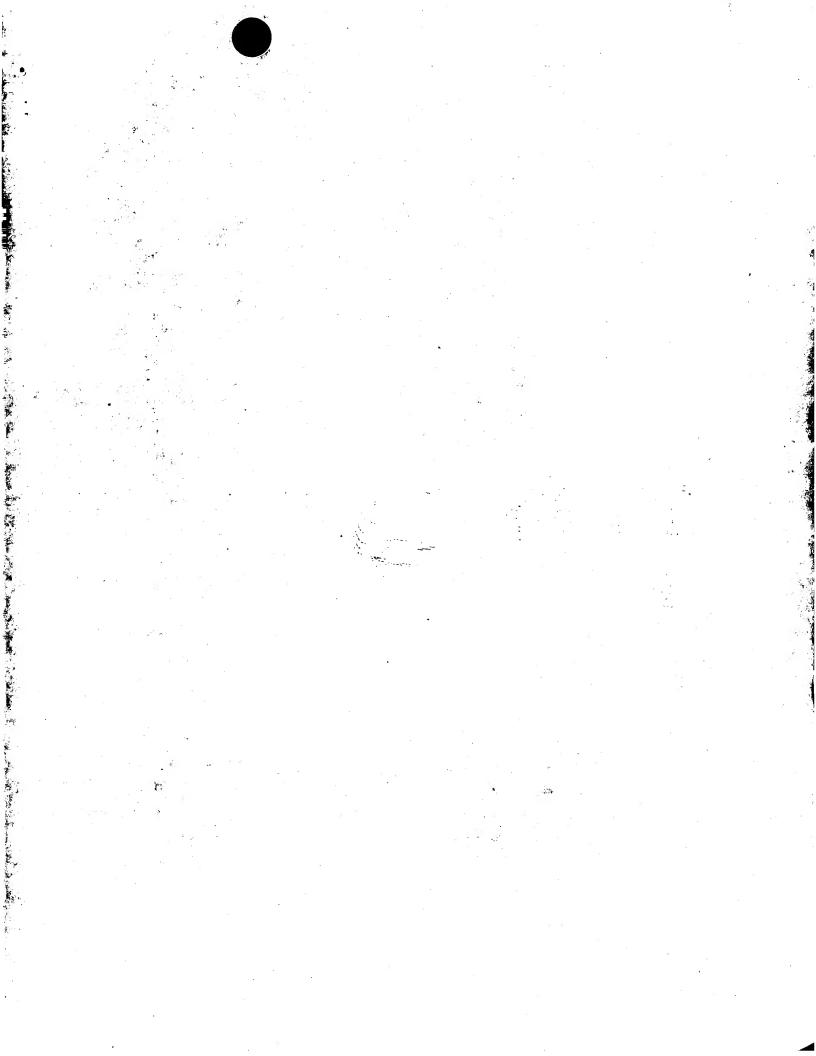
COFACTOR: CAN USE BOTH NAD OR NADP.
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PF00479; G6PD; 1.
PF01182; Glucosamine_iso;
PF02781; G6PD_C; 1.
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                                                                                                                                                                                                                                                                                                                                Zealand white; TISSUE-Liver; 281746; PubMed-8506377;
                                                                                                                                                                                                                                                                                                                                                                                                                cuniculus (Rabbit).
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a; Leporidae; Oryctola;
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DOMAIN
ACT_SITE
CARBOHYD
CARBOHYD
Development 105:299-307(1989).

-!- FUNCTION: DESMIN ARE CLASS-III INTERMEDIATE FILAM MUSCLE CELLS. IN ADULT STRIATED MUSCLE THEY FORM NETWORK CONNECTING MYOFIBRILS TO EACH OTHER AND TMEMBRAME FROM THE PERIPHERY OF THE Z-LINE STRUCTU-!- SUBUNIT: HOMOPOLYMER.
                                                                      SEQUENCE FKUM N.A.
MEDLINE=90032404; PubMed=2806128;
Herrmann H., Fouquet B., Franke W.W.;
"Expression of intermediate filament proteins dur
                                                                                                                                                   Eukaryota; Metazoa; Chordat; Amphibia; Batrachia; Anura; Xenopodinae; Xenopus.
                                                                                                                                                                                               DES.
                                                                                                                                                                                                                             01-NOV-1991
01-NOV-1991
                                                                                                                                                                                                                                                  DESM_XENLA P23239;
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MOD_RES
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                                                                 desmin.",
                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                        NCBI_TaxID-8355;
                                                                                                                                                                                   Xenopus laevis (African
                                                                                                                                                                                                        Desmin.
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Matches 49; Conserv
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SITE
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A43554; A43554.
InterPro; IPRO01664; IF.
Pfam; PP0038; filament; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Muscle protein.
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-1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
357 -RLEEEIRNMKDEMARHLREYQ 377
                                180 AEAQEEFLRVLGSMCQRLRSMQ 201
                                                                      301 AMROSKOEMMEYRHOIOS----YTCEIDALKGTNDSLMRQMRDLEEKFSGEAAGYODTIG 356
                                                                                                                                                                                                                    183 QEEIQLKEDAENNLAAFRGDVDAATLARIDLERRIESLQEEI-AFLKKIHEEEIRELQAQ 241
                                                                                                        143 ------SYLREVSSYPSTVG 179
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                                                                                                                                                                                                                                                                                                                                                                       458 AA;
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                                                                                                                                                                                                                                                                                                                                                                     52802 MW;
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COIL 1A.
LINKER 1.
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LINKER 12.
COIL 2B.
LINKER 2.
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Jearch completed: May 26, 2003, 15:21:38 Job time: 23 secs



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Result
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N-PSDB; AAZ38992.	₽ .	Wang X, Liu X;	(TEXA) UNIV TEXAS SYSTEM.	16-APR-1998; 98WO-US07895.	16-APR-1998; 98WO-US07895.	28-OCT-1999.	WO9954482-A1.	Homo sapiens.	cytostatic; growth; tumour.	Human; DNA fragmentation factor; DFF40; DFF45; apoptosis; gene therapy;	Human DNA fragmentation factor DFF40 protein sequence.	22-FEB-2000 (first entry)		AAY57440;	RESULT 1 AAY57440 ID AAY57440 standard; Protein; 338 AA.	

XPTXRR

DNA fragmentation factor DFF40 involved in apoptosis and related polynucleotide

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                                                                                                                                                        molecular chaperone;
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                                                                                                                                                                       fragmentation factor; DFF40; DFF45; apoptosis; DNase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of a cancer
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ilarity 100.0%;
Conservative
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2842-006-5486
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                                                                                                                                                      cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represents a human DNA fragmentation factor so described are: (1) a method of inducing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell,
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                                                                                                                                                                                                                                                                                                    338
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                                                                                                                                                                                                   DNA fragmentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    especially in humans.
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Pred. No. 8.8e-167;
Mismatches 0;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang X,
AAY72467 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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)B; AAH74642.
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                                                                             LVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ 338
                                                              LVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ
                                                                                                              INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK 300
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llarity 100.0%;
Conservative 0
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338
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Pred. No. 8.
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d.8e-167;
es 0;
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AAY72467
ID AAY72467;
XX
AC AAY72467;
XX
DT 24-APR-2001 (first entry)
XX
KW
Human DNA fragmentation factor 40 (DFF40).
XX
KW
gene therapy; hyperproliferative disorder; therapy; tumour; restenosis; KW
psoriasis; angiogenesis; cancer; cytostatic; neoplasia.
XX
OS Homo sapiens.
XX
PD 26-DEC-2000.
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RESULT 4
AAY04123
ID AAY
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AC AAY
AC AAY
XX
DT 11-
XX
DE Cas
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying modulator of human DNA fragmentation factor 40, for treating cancer, involves contacting cell or cell-free composition comprising DFF40 with candidate substance and comparing apoptosis with control
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N-PSDB; AAD02498.
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  Caspase activated nuclease CPAN
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                                        11-JUN-1999
                                                                                 AAY04123;
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llarity 100.0%;
Conservative 0
                                      (first entry)
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Pred. No. 8.8e-167;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JAN-1998;
22-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated caspase activated nuclease - used to develop products which can inhibit or activate apoptosis for use in treating e.g. heart attack, stroke or tumours
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                             301 LVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ 338
                                                              241 INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                              338 AA;
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97US-0056904.
97US-0056907.
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Pred. No. 1.7e-166;
1; Mismatches 0;
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Best Local Sin
Matches 261;
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         AAY29936 standard; Protein; 344 AA
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibitor for caspase-activating DNase - useful for preventing death and is useful as reagent for cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-554024/47.
N-PSDB; AAZ21173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; caspase activating DNase; cell death.
                                                                                                                                                                                                                                                                                                                                                                                                               Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP11239495-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse caspase-activating DNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY29931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY29931
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                                                                                                                                                                                                                                                                                                Similarity
                                                                   LVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ
                                                                                                                                             EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS
                                                                                                                                                                                 DLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGA 180
                                                                                                                                                                                                           MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                       INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK
                                                                                                                                                                      DLLHHVSQNITAETREQDPSWFEGLESRFRNKSGYLRYSCESRIRGYLREVSAYTSMVDE 183
                                                                                                                                                                                                                                                                                                                                                                                                              Page 16-17;
                                                        LVHIACHKKTTHKLECDRSRIYRPQTGSRRKQPARKKR
                                                                                            INPYGNRESRILFSTWNLDHIIEKKRTVVPTLAEAI--QDGREVNWEYFYSLLFTAENLK
                                                                                                                                  AAQEEYLRVLGSMCQKLKSVQYNGSYFDRGAEASSRLCTPEGWFSCQGPFDLESCLSKHS
                                                                                                                                                                                                                              PSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLA 120
                                                                                                                                                                                                                                                                                    79.2%;
nilarity 77.2%;
Conservative 3
                                                                                                                                                                                                                                                                                                                           344 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344
                                                                                                                                                                                                                                                                                      Score 1416; DI
Pred. No. 3.6e
37; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibitor; ICAD; ICAD-L; ICAD-S;
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RESULT 7
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Matches 261;
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Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents mouse caspase activating DNase (CAD). CAD can be used for the removal of cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 14-15;
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                               06-NOV-2001
                                                            AA009550;
                                                                                        AAO09550 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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N-PSDB; AAZ21180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; caspase activating DNase; CAD; cell death; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse caspase activating DNase
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                                                                                                                                                                                                                                                                                   184 AAQEEYLRVLGSMCQKLKSVQYNGSYFDRGAEASSRLCTPEGWFSCQGPFDLESCLSKHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                    LVHIVCHKKTTHKLNCDPSRIYKPQTKLKRKQPVRKRQ
                                                                                                                                                                                                                                                                                                                                                                                                 LVHIACHKKTTHKLECDRSRIYRPQTGSRRKQPARKKR
                                                                                                                                                                                                                         INPYGNRESRILFSTWNLDHIIEKKRTVVPTLAEAI--QDGREVNWEYFYSLLFTAENLK
                                                                                                                                                                                                                                          INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK
                                                                                                                                                                                                                                                                                                                  EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLRQPKCVKLRALHSACKFGVAARSCQELLRKGCVRFQLPMPGSRLCLYEDGTEVTDDCF
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                             (first
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 SEQ ID NO 23442.
                             entry)
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Pred. No. 3.6e-130;
7; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibitor; ICAD;
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cell proliferation;

cell differentiation;

gene

therapy;

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RESULT 8
ABB6436
ID ABB6
XX ABB6
XX ABB6
XX 26-M
XX 26-M
XX Dros
XX Dros
XX Dros
XX Dros
XX Dros
XX Dros
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est Local S
tches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proteins or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis and/or activity, insunomodulatory activity and may be useful in the diagnosis and/or the telement of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation.
                                                                    Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 23442; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun disorders -
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                       Drosophila melanogaster
                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 20010.
                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                           ABB64406 standard; Protein; 450 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                              294 FTSENLKLVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ 338
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76; Conserv
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Pred. No. 1.4e-28;
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AAY92335
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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11-JUL-2000; 2000US-0614150
                       AAY92335 standard; Protein; 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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(ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 20010; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid
genes from Drosophila and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY.
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Interactions -
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                                                                                                                                     400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 P--DAVITTDADFEFEKMRQQSPLLKVA-DIFYDFIEQHPEKFRRMITEYEHQKQRRVLD 171
                                                                                                                                                                                                                                                                                                               281 RIPSKRLRQVIREYTKENCILDEWSTSLCSDLGDFYCQGSYSENGNSCSKQHTINPYASR 340
                                                                                                                                                                                                                                                                                                                                                                                                      221 TRNPLYRQNAKARQVINSVLEKFRYLLIGCDFFSMMFDRNCKQKHEFLKQHLGDEETDAG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 NSKTHLSLKAEHVEWFTGGEERFHSKEEAMATRAQTRVRGYY-----YKAKEEL 220
                                                                                                                                                                            294 FTSENLKLVHIVCHKK-----TTHKLNCDPSRIYK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 QAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCD--EQAPQR-QRLLADLLHNVSQNIAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 RKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTED-YFPSVPDNAELVLLTLG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                  FSLKNLKLVHIVCHEKAQRSNRSNGRLLCSDCHEYR 435
                                                                                                                                                                                                                         ENLILFQVWNLDHQIELCRTILPALVANVEELYSHPQTKCSIHKKQVVDISVLEYFLE-I 399
                                                                                                                                                                                                                                                                                                                                                         RKYGIGANSLEMLIAKAKSKFPLLE--PHLYLASDGFEVSDDEYLKSLP--AQTLFIVSG 114
                                                                                                                                                                                                                                                                     ESRILFSTWNLDHIIEKKRTIIPTLVEAIKE------QDGREVD---WEYFYGLL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              450 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 321; DB 22;
Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
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                                                                                                                                                                                                                                                                                                    PXR
                                                                                                                                                                                                                                                                                                                                                                                        14-3-3epsilon, alpha-tropomyosin, vimentin, p0071, Ini-1, IP-1, IP-2, IP-3, IP-4, or IP-5. NIK1 (also referred to as Nek2) is a human homologue of the Aspergillus nidulans mitotic regulator, NIMA kinase. NIK1 is a serine/threonine-specific kinase and is thought to play a k role in cell-cycle events leading to the onset of mitosis. The complexes, their derivatives and NIK1 or NIK1-IP protein and DNA
                                                                                                                                                                                                                                                                                                                                       sequences, etc. are useful for treating or preventing a disease or disorder involving aberrant levels of the complex or protein. Such disorders include cancer, hyperproliferative disorders, neurodegenerative disorders, cardiomyopathies, viral infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New complex of a NLK1 protein and a NLK1 protein-interacting protein, useful for treating cancer, hyperproliferative disorder, neurodegenerative disorder, cardiomyopathies, viral infections and metabolic disorders
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                             metabolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interacting proteins. The invention concerns purified complexes of NLK1 protein and a NLK1 protein interacting protein, where the interacting protein is chosen from TrkA, protein phosphatase lalpha, interacting protein is chosen from TrkA, protein phosphatase lalpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY92331-37 were isolated in a modified yeast two hybrid system using NNK1 protein as "bait". These are known sequences which are NNK1 interacting proteins. The invention concerns purified complexes of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA09307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI: 2000-303742/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nandabalan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiviral; neuroprotective; cardiant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human vimentin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NlK1 Interacting Protein; vimentin; protein complex; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 145-147; 172pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-2000
                                                                                                                                                                                                                                                                         Match
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                                                     167
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  227
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                                                                                                                                                                                                                    27
                                                                                                                                                                                                                                                          Similarity
                                                    YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC 226
                                                                                                                                  AFLKKLHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
                                                                                                                                                             RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141
                                                                                                                                                                                      EDIMR----LREKLQEE----MLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEI- 231
                                                                                                                                                                                                              QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR
 QGPFDMDSCLSRHSINPYSNRESRIL --
                         FAVEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ---
                                                                                YKSKFADLSEAANRNNDALRQAKQESTEYRRQVQSLTCEVDALKGTNESLERQMREMEEN
                                                                                                                                                                                                                                                                                                   466 AA;
                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schulz
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                                                                                                                                                                                                                                                          5.5%;
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                                                                                                          -EGLESRFQSKSGYLRY--
                                                                                                                                                                                                                                               47;
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                                                                                                                                                                                                                                                          Score 99; DB 21; Pred. No. 0.9;
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                                                                                                                                                                                                                                             Mismatches
---FST----
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-WNLDHI---
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-IEKKRTIIPTL
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RESULT 10 · AAB66349 ID AAB66
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Best Local
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systemic l
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides an antibody which reacts with a cleavage product of vimentin but not with the intact protein. This can be used to detect apoptosis, which may then be used as an indicator of the progression of diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, Basedow's disease and acquired immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibody reacting with a cleavage product of vimentin but not with the intact vimentin, useful for detecting apoptosis and the quantity of cleavage product of vimentin or as a reagent for immunohistochemical
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     syndrome (AIDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine vimentin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB66349 standard; peptide; 466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RIKE ) RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-2001
                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                    142
                                                                                                                                                                                                                                     180 EDIMR----LREKLQEE-----MLQREEAESTLQSFRQDVDNASLARLDLERKVESLQEEI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-149349/16
                                      167 YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC
                                                                               291
                                                                                                                                                         232 AFLKKLHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444
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                                                                                                                                                                                                                                                                             27
                                                                                                                                                                                            87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW
                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                     Similarity
FALEAANYODTIG-RLQDEIQNMKEEMARHLREYQ--
                                                                                                                                                                                                                                                                         QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEAIKEQDGREVD
                                                                             YKSKFADLSEAANRNNDALRQAKQESNEYRRQVQSLTCEVDALKGTNESLERQMREMEEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caspase cleavage site; apoptosis; antibody; Basedow's
lupus erythematosus; autoimmune haemolytic anaemia; AII
                                                                                                                                                                                                                                                                                                                                                                                                466
                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              AA;
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20.1%;
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                                                                                                                    -EGLESRFQSKSGYLRY---
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                                                                                                                                                                                                                                                                                                                                     Score 99; DB Pred. No. 0.9;
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                                                                                                                                                                                                                                                                                                                                                       Length 466
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                                                                                                                  SCESRIR----S
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-DLLNV
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RESULT 11
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                                                                                                                                                                                          The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB159202 to AB159912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression profile or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAR-2002
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                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 2178-2180; 2690pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-034733/04.
N-PSDB; ABI99777.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse ischaemic condition related protein sequence SEQ ID NO:867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB57310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishikawa K, Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 KMALDIEIATYRKLL---EGEESRISLPLPTFSSLNLRETNLESLPLVDTHSKRTL---L 443
                                            180 EDIMR---LREKLQEE----MLQREEAESTLQSFRQDVDNASLARLDLERKVESLQEEI 231
                                                                         27 QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86
87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141
                                                                                                         63;
                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGPFDMDSCLSRHSINPYSNRESRI-----LESTWNLDHI------IEKKRTIIPTL 272
                                                                                                                                                                    466 AA;
                                                                                                      5.5%; Score 99; DB 23; Length 466; Conservative 47; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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RESULT 12
AAW54351
ID AAW54
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AC AAW54
XX
                              Query Match
Best Local :
                                                                                                                                                          Proteins AAW54349-W54364 are examples of proteins produced in the endometrium during the hyperplasia, adenocarcinoma or proliferative phase of the endometrium. The presence and quantities of these proteins can be detected using 2D gel electrophoresis comparison of cell lysates. The proteins can be used as biochemical markers to detect the phase of the endometrium and can be measured in body fluids, obviating the need for endometrial biopsies.
                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemical markers of human endometrium - useful for, diagnosis of hyperplasia and adenocarcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-207057/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Byrjalsen I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-APR-1997;
06-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
2D gel electrophoresis; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vimentin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW54351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW54351 standard; protein; 465 AA
                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 20; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CLIN-) CENT CLINICAL & BASIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 YKSKFADLSEAANRNNDALRQAKQESNEYRRQVQSLTCEVDALKGTNESLERQMREMEEN 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 VEAIKEQDGREVD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 KMALDIEIATYRKLL---EGEESRISLPLPTFSSLNLRETNLESLPLVDTHSKRTL---L 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 F-----SCESRIR----S 166
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   1 Similarity 20.8%;
65; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGPFDMDSCLSRHSINPYSNRESRI-----LFSTWNLDHI-----IEKKRTIIPTL 272
                                                                                                               465 AA;
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96GB-0018600.
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Score 97; DB 19; Length 465; Pred. No. 1.4; 16; Mismatches 112; Indels
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179 EDIMR----LREKLQEE-----MLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEI- 230

27 QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86

46;

90;

Gaps

87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141

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9635
AAB29635 standard; Protein;
The invention relates to the human pollinosis-associated gene 795 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 795 has homology with the human vimentin gene. The invention also relates also relates to the protein encoded by pollinosis gene 795; to expression constructs and host cells comprising pollinosis-associated gene 795 nucleic acids; pollinosis-associated gene 795 primers and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 795 nucleic acids; and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 795 nucleic acids. The invention additionally encompasses methods of
                                                                                                                                                                                                                                                                                                                                                                                                                (GENO-)
                                                                                                                                                                                                                                                bollinosis-associated in subjects with high diagnosis of allergic
                                                                                                                                                                                                                                                                                                          WPI; 2000-687343/67.
N-PSDB; AAC64226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; pollinosis-associated gene 795; vimentin homologue; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
                                                                                                                                                                                                                                                                                                                                                                     Obáyashi I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-NOV-2000
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                                                                                                                                                                                                                      Page 64-67; Claim 13;
                                                                                                                                                                                                                                                                                                                                                         Yokoi A;
                                                                                                                                                                                                                                                                                                                                                                                     Nagasu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-2000; 2000WO-JP02734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection; diagnosis;
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                                                                                                                                                                                                                                             gene 795 undergoing significantly low expression cedar pollen-specific IgE levels, useful in diseases and screening drug candidates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug screening; allergic disease.
                                                                                                                                                                                                                   73pp; Japanese.
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Yoshida N, Ogawa K, Matsui K, Takahashi E;
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New antibody reacting with a cleavage product of vimentin but the intact vimentin, useful for detecting apoptosis and the que cleavage product of vimentin or as a reagent for immunohistoch

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2001-149349/16

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Best Local S
Matches 65
                                                                                                                                                                       Vimentin;
systemic 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    screening drug candidates for the treatment of allergic disease measuring the expression of pollinosis-associated gene 795 in pollinosis-associated gene 795 in pollinosign-stimulated T-cells in the presence of a test compound reaction. Pollinosis-associated gene 795 is useful in the diagnallergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a protein encoded by human pollinosis-associated gene 795.
                                                                                                                                                                                                             Human vimentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
 Morishima
                        (RIKE ) RIKEN
                                                 07-JUL-1999;
                                                                         07-JUL-2000; 2000EP-0305736
                                                                                                  10-JAN-2001
                                                                                                                          EP1067142-A1
                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                     AAB66348 standard;
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'n
                                                                                                                                                                       caspase cleavage site; apoptosis; antibody; Basedow's dis
lupus erythematosus; autoimmune haemolytic anaemia; AIDS;
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Nakanishi
                                                  99JP-0193235
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Shibata
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Pred. No. 1.4;
46; Mismatches
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                                                                                                                                                                07-AUG-2000; 2000US-223130P.
30-JAN-2001; 2001US-265447P.
15-MAY-2001; 2001US-291201P.
                                                                                                                                                                                                                                                                                                                  WO200212331-A2.
                                                                                                                                                                                                                                                                                                                                                                                      Human; pancreatic tumour protein; immune response; pancreatic cancer; development of cancer; cancer progression; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human pancreatic tumour protein #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU87694;
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                                                                                            Pyle RA, Xu J, Kalos
                                                                                                                                                                                                                                           06-AUG-2001; 2001WO-US24619
                                                                                                                                                                                                                                                                                14-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
Novel polynucleotide encoding pancreatic tumour polypeptides, useful in
                                      N-PSDB; ABK44209.
                                                       WPI; 2002-241741/29.
                                                                                                                                (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC
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RESULT 16 AAM79837

AAM79837 standard; Protein; 1152 AA

06-NOV-2001 (first entry)

Human protein SEQ ID NO 3483.

AAM79837;

PD XXX

WO200157190-A2

Homo sapiens.

Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;

nervous system disorder; arthritis; inflammation.

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Best Local S
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AAU87689-AAU87694 represent human pancreatic tumour proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the isolation of cDNA sequences (ABK44061-ABK4209) encoding human pancreatic tumour proteins. The polynuclectide sequences encoding human pancreatic tumour proteins are useful for stimulating an immune response in a patient and treating pancreatic cancer in a patient. A host cell that expresses these polynuclectides is useful for determining the presence of cancer in a patient.
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444 IKTVETRDGQVIN 456
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                                                                                                                                          227 QGPFDMDSCLSRHSINPYSNRESRIL-----FST-----WNLDHI----IEKKRTIIPTL 272
                                                                                                                                                                                         351 FAVEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ------
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Zhao QA,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
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N-PSDB; AAK52970.
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27-APR-2000;
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20-OCT-2000;
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19-JUL-2000;
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, Wang D,
Yang Y,
CHKKTTHKLNCDPSRIYKPQTRLKRKQPVRK
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                                                                          RELENYTDCPELYGRCFLERMEDFQIYEKYCQNKPRSESLWRQCSDCPFFQE----
                                                                                                                                                                      ----ELLCVLEGYAA-----EMDNPLMAHLLSTGLHNKKDVLFG--NMEEIYHFHNRIFL
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2000US-0693325.
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2000US-0620325.
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Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
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Pred. No. 9.4;
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F, C
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Wang,
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4 KPKSVKLRAL-----RSPRKFGVAGRSCQ----EVLRKGCLR--FQLPERGSRLCLYE 50

Indels

RPKCQELRHLCDQFSAEIARRRGLLSKSLELHRRLETSMKWCDEGIYLLASQPVDKCQSQ

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                         Query Match
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Zhao QA,
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15-SEP-2000;
20-OCT-2000;
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27-APR-2000;
20-JUN-2000;
                                                                                                                                                               The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating
                                                    Sequence
                                                                           Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                               activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis an
                                                                                                                                                                                                                                                                         Claim 20; Page 3811-3813; 6221pp; English.
                                                                                                                                                                                                                                                                                                 useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                Nucleic acids encoding polypeptides with cytokine-like
                                                                                                                                                                                                                                                                                                                                        WPI; 2001-476283/51.
N-PSDB; AAK51986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; vacchie; peptide therapy; stem cell growth factor; haematog tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human protein SEQ ID NO 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM78853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM78853 standard; Protein; 1120
                                                                                                                                                                                                                                                                                                                                                                                 Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157190-A2
                                                                                                                    inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2000;
              Local
             Similarity
                                                                                                                                                                                                                                                                                                                                                                              Liu C,
Wang D,
Yang Y,
                                                    1120 AA;
 Conservative
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2000US-0654936.
2000US-0663561.
2000US-0693325.
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2000US-0598075
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                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT,
Wang J, Zi
                                                                                                                                                                                                                                                                                                                                                                               Wejhrman T,
            5.2%;
                                                                                                                                                                                                                                                                                                                                                                                            Zhang
            Score 93.5;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                              Asundi V,
mang J. Re
                                                                                                                                                                                                                                                                                                                                                                               Goodrich
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             Ren
                         В
                                                                                                                                                                                                                                                                                                                                                                                                      Zhou
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 155;
                                                                                          2111
from
                         22;
                                                                                                                                                                                                                                                                                                                                                                                            Chen
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                         Length 1120;
                                                                                       (AAK52582) and 3666 the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                          R, C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                          Wang
                                                                                                                                                                                                                                                                                                                                                                                                      Cao Y,
 99;
                                                                                                                                                                                                                                                                                                                                                                                            ZW;
                                                                                         listing
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     PSX PPTX X PTX X 
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                       Tang YT,
Wang J,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                              WPI; 2001-442253/47.
N-PSDB; AAI59957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM40801 standard; Protein; 181 AA.
Example 2; SEQ ID NO 5732; 10078pp; English
                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                           (HYSE-)
                                                                                                                                                                                                                                                                                                                                                          29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polypeptide SEQ ID NO 5732.
                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               777 CORKLDHKLSLD-SYLLKPVORITKYQLLLK 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             725 RELENYTDCPELYGRCFLERMEDFQIYEKYCQNKPRSESLWRQCSDCPFFQE-----
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                                                                                                                                                                                                 Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                        HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHKKTTHKLNCDPSRIYKPQTRLKRKQPVRK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---KKRTIIPTLV------EAIKEQDGREVDWEYFYGLLFTSENLKLVHIV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGALRRGPYRRAKSEVSESRQGRGSAGEE--EESLAILRRHVMSELLDTER---AYVE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGYLRYSCESRIRSYLREVSSYPSTVGAEAQEEFLRVLGS--MCQRLRSMQYNGSYFDRG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROASLKKLAAROTRPVOPVAPRPEAL------AKSPCPSPGIRRGSENS-SSE 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGAEAALQEIEKFLETGAENKIQELNAIYKEYESILNQDLMEHVRKVFQKQASMEEVFHR 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKGGSRLCTPEGWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ELLCVLEGYAA-----EMDNPLMAHLLSTGLHNKKDVLFG--NMEEIYHFHNRIFL
                                                                                                                                                                                                                                                                                                                                                    2000US-0488725.
2000US-0553317.
2000US-0598042.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0663191.
2000US-0693036.
2000US-0727344.
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                                                                                                                                                                                                 Asundi V, Ch
Wehrman T, X
Goodrich R,
                                                                                                                                                                                                                              Chen R,
                                                                                                                                                                                                       nen R, Ma Y,
tu C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                           Qian XB,
Yang Y,
                                                                                                                                                                                                                              Ren F, 1
Zhang J;
                                                                                                                                                                                                                                                   Wang D;
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RESULT 19
AAU03204
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Best Local
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/label= OTHER /note= "Other= Misc-difference 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAA38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathys and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                     HLYAL47; CIDE; Cell death inducing DFF45-like effector; apoptosis; programmed cell death; cancer; haematological dibone marrow failure; myelodysplastic syndrome; aplastic ana neutropaenia; leukaemia; cardiovascular disease; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                             Misc-difference 124
                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                              Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CIDE protein consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU03204 standard; Protein; 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.N.S disorders. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                            Mus sp
                                                                                                                                                                                                                                                                                                                                                                                  reperfusion; liver disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU03204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 S----YPSTVGAEAQEEFLRVLGS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 RORLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLR--EVS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 PDFGPSSFVP-----SWGATATGARKFLIAFN---INLLGTKEQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALHTYYEETC-REAQELSLPVVGS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AHRIALNLREQGRGKDQP---GRLKKVQGIGWYLDEKNLAQVSTNLLDFEVT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDYFPS--VPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF--PE---RTCSQLQQADWA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                      note= "Other= unknown"
                                                                                                                                                                        label- OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.2%; Sc
24.5%; Pr
ative 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 93;
Pred. No.
                                                        unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; haematological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 86;
                                                                                                                                                                                                                                                                                                                                                                               neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76;
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Misc-difference

/label= OTHER

note- "Other-

unknown"

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RESULT 20
ABG04580
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a CIDE (Cell death inducing DFF45-like effector) consensus sequence, thought to be involved in apoptosis and programmed cell death. Human HLYAL47 polypeptides (a CIDE B protein) and polynucleotides are useful in the treatment of cancer, haematological disorders, e.g., bone marrow failure including myelodysplastic syndromes, aplastic anaemia, neutropaenia and leukaemia, cardiovascular diseases (e.g. ischaemia and reparrusion), liver diseases, inflammation and neurodegenerative pathologies. These may also be used as research reagents and materials for the discovery of treatments and diagnostics for animal and human diseases, for chromosome identification, as immunogens to produce HLYAL47 specific antibodies, and in screening for (ant)agonists of the HLYAL47 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New HIYAL47 polypeptides and polynucleotides, useful for treating cancer, hematological disorders, bone marrow failure such as myelodysplastic syndromes, aplastic anemia, neutropenia and leukemia,
             Human; chromosome mapping;
food supplement; medical ir
                                                        Novel human
                                                                                     13-FEB-2002
                                                                                                                                            ABG04580 standard; Protein; 214 AA
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grailhe P,
            food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiovascular diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SNFI ) SANOFI-SYNTHELABO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1999;
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                                                                                                                                                                                                                     104 EKGQSW 109
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                                                                                                                                                                                                                                                                            45
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                                                                                                                                                                                                                                                                                                                                      27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                              221 AA;
                                                      diagnostic protein #4571
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          imaging;
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maging; diagnostic; genetic disorder
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Search completed: May 26, Job time: 57 secs

2003, 15:21:03

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                                                                                                                                                        Matches
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Best Local :
                                                                                                                                                                                                                                                                                      diagnostic amino acid sequences of the invention Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                  Sequence
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23-AUG-2000; 2000US-0649167
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106 EYFQALAGDTVFMVLQKGQKWQPPSEQGTRHPLSLSHKP 144
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                                      DYFPSVPDNAELVLLTLGQAWQ-GYVSDIRRFLSAFHEP
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and is derived by analysis of the total score distribution.
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AF409062 Homo

AB013918 Homo sapi AR122560 Sequence

Homo sapi Homo sapi Homo sapi

Description

AF149797 Drosophil
AB036773 Drosophil
AL806525 Mus muscu
AC009340 Drosophil
AE003659 Drosophil
AC012906 Drosophil
AC012906 H.saplens v
BC030573 Homo sapi
AL603906 Human DNA

U05823 Mus musculu AJ002156 Pinus str AF136601 Rattus no AE002394 Neisseria Continuation (23 o AL512292 Leishman 1 AL162758 Neisseria AX044029 Sequence AF032688 Oryza sat AC129718 Oryza sat AC129718 Oryza sat AC124011 Mus muscu M20384 Pui apolipo X96391 H.sapiens m M25246 Human vimen

Database :

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Mammalia; Eutheria;
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                                      GluArgGlySerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPhe
                                                                                        ValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuPro
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                                                                            GTGGCTGGCCGGAGCTGCCAGGAGGTGCTGCGCAAGGGCTGTCTCCGCTTCCAGCTCCCT
ProSerValProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGly
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/protein_id="BAA32250.1"
/db_xref="GI:3410909"
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AQQLLCDGAPAPQRQRLADLLHNVSQNIAASTRAEDPPWFEGLESRFQSKSGYLRYSC
ESRIRSYLREVSSYPSTVGABAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLC
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/product="CAD"
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                                                               GlyArgGluValAspTrpGluTyrPheTyrGlyLeuLeuPheThrSerGluAsnLeuLys 300
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                                      GGAAGAGAAGTGGACTGGGAGTATTTTATGGCCTGCTTTTTACCTCAGAGAACCTAAAA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutexternative Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2839)

Liu,X., Li,P., Widlak,P., Zou,H., Luo,X., Garrard,W.T. and The 40-kba subunit of DNA fragmentation factor induces DNA fragmentation and chromatin condensation during apoptosis fragmentation and chromatin condensation during apoptosis fragmentation and Sci. U.S.A. 95 (15), 8461-8466 (1998)
    Similarity:
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Liu, X. and Wang, X.
Direct Submission
Submitted (07-MAY-1998) Biochemistry, [
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AQQILICDEQAPQRQRILADILHNVSQNIAAETRAEDPPWEBGIESRFQSKSGYIRYSC
ESRIRSYLKEVSSYPSTYGAEAQEEFLEVLGSMCQRIRSMCYNGSYFDRGAKGGSRIC
TPEGWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAI
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/product="DNA fragmentation factor 40 kDa subunit"
/product="DNA fragmentation factor 40 kDa subunit"
/protein_id="AAC39920.1"
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/db_xref="taxon:9606"
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/db_xref="GI:3347857"
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/function="nuclease;
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hromatin condensation during apoptosis"
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AF039210
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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1017)
                                              Homo sapiens.
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Williams,L.T.
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                                                                                     TATGTGAGCGACATCAGGCGCTTCCTCAGTGCATTTCACGAGCCACAGGTGGGGCTCATC
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Horton Street, Emeryville, CA 94608, USA
Location/Qualifiers
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RLCLYEDGTELTEDYFESYPDINAELVLLTLGQAWQGYVSDIRFLSAFHEPQVGLIQA
AQQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPFWFEGLESRFGSKSGYLRYSC
ESRIRSYLREVSSYPSTYGAEAQCEFLRVLGSWCQKLRSMQYNGSYFDRGAKGGSRLC
TPEGWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIFTLVEAI
KEDDGREVDWEYFYGLLFTSENLKLVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPV
RKRQ"
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/protein_id="AAC39709.1"
/db_xref="G1:3056727"
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/db_xref="taxon:9606"
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                                                                           Direct Submission
Submitted (Gr-JUN-1999) Akira Nakagawara, Chiba Cancer Center Research Institute, Division of Biochemistry; 666-2 Nitona, Chubh-ku, Chiba, Chiba 260-8717, Japan (E-mail-akiranakéhiba-cc.pref.chiba.jp., Tel:81-43-264-5431(ex.5201), Fax:81-43-265-4459)
                                                                                                                                                                                                                                                                                                                              AB028913.1 GI:13516478
DNA fragmentation factor 40 kDa subunit delta; DNA fragmentation factor 40 kDa subunit.
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                                                                                                                                                                         Nakagawara,A.,
                                                                                                                                                                                      Published Only in DataBase (2001) 2 (bases 1 to 2926)
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 /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="Neuroblastoma"
                                                               Location/Qualifiers
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Mammalia; Eutheria;
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ESRIRSYLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDDGAKGGSRLC
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1 (bases 1 to 1028)
1 Bayascas, J.R., Yuste, V.J., Perera, R. and Commella, J.X.
Characterization of splice variants of human caspase-activated DNase that show CIDE-N structure and function
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/db_xref="GI:1553729"
/translation="MLQREKSVKLRALRSPRKFGVAGRSCOEVLRKGCLRFQLPERGS
/translation="MLQREKSVKLRALRSPRKFGVAGRSCOEVLRKGCLRFQLPERGS
RLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAMQGCGRCERHQALPQCISRATGGAH
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/db_xref="taxon:9606"
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218 sThrProGluGlyTrpPheSerCysGlnGlyTrpPheSerCysLeuSerAr
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DNA fragmentation factor B truncated form II (DFFB)
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Bayascas, J.R., Yuste, V.J., Perera, R. and Comella, J.X.
Characterization of splice variants of human caspase-activated
DNase that show CIDE-N structure and function
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 uThrArgAlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSe
                                                                                         CCCAGTGTTCCCGACAACGCCGAGCTGGTGCTGCTCACCTTGGGCCAGGCCTGGCAGGGC
                                                                                                                                                                                                                                                                       GAGCGCGGTTCCCCGGCTGTGCCTGTACGAGGATGGCACGGAGCTGACGGAAGATTACTTC
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(bases 1 to 1043)
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TGGAHPGRPAAAV"
1 296 c 314 g 191 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="DNA fragmentation factor B truncated form II"
/protein_id="AALIO2006.1"
/db_xref="Gi:1553731"
/translation="MIQKPKSVKLRALRSPRKFGVAGRSCOEVLRKGCLRFQLPERGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="IMR-5"
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|. .1043
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                                                                                                                                                             2 (bases 1 to 1071)
Comella, J.X., Bayascas, J.R.,
                                                                                                                                                                                                         Bayascas, J.R., Yusté, V.J., Perera, R. and Comella, J.X. Characterization of splice variants of human caspase-activated DNase that show CIDE-N structure and function
                                                                                                                                                                                                                                                                                                                                                                                      AF409062 1071 bp mRNA linear Homo sapiens DNA fragmentation factor B truncated
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ted (13-AUG-2001) Ciencies Mediques Basiques,
t, Av. ROVITA ROUTE 44, Lleida 25198, Spain
          /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="IMR-5"
/cell_type="neuroblastoma"
1 1071
/gene="DFFB"
                                                                                                      ocation/Qualifiers
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164 IleArgSerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGln 183
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//db_xref="GI:15559733"
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RICIXEDGTELTEDYFFSVPDNAELVLLTLGQAWQG"
a 306 c 319 g 204 t

    247
    /gene="DFFB"
    /note="CIDE-N-only protein; alternatively spliced"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (11-JUN-1999) Akira Nakagawara, Chiba Cancer Center Research Institute Division of Biochemistry; 666-2 Nitona, Chubh-ku, Chiba, Chiba 260-8717, Japan (E-mail:akiranakehiba-cp.pref.chiba.jp. Tel:81-43-264-5431(ex.5201), Fax:81-43-265-4459)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABO28912 3008 bp mRNA linear [PRI 03-APR-2001] Homo sapiens DFF40 gamma mRNA for DNA fragmentation factor 40 kDa subunit gamma, complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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C12N15/09,C07K16/40,C12N5/10,C12N9/22,C12N15/00,C12N5/00
Key Location/Qualifiers
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                                                                                                                                                                                        OSAKA BIO SCI KENKYUSHO
OS HOMO Sapiens (human)
PN JP 199233495-A/1
PD 17-SEP-1993
PF 25-DEC-1998 JP 19983
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PC C12P21/08//(C12N15/09,C12R1:91),(C12N1/21,C12R1:19)
(C12P21/02, PC C12R1:19),
PC C12N15/00,C12N5/00,(C12N15/00,C12R1:91)
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                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1038) Shigekazu, N. and Masato, E.
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Homo sapiens
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                                                                                                            SHIGERAZU NAGATA, MASATO ENARI
C12N15/09,C07K14/81,C07K16/18,C12N1/21,C12N5/10,C12N9/99,
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Sakahira.H., Enari,M. and
Cleavage of CAD inhibitor
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CAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enari,M., Sakahira,H., Yokoyama,H., Okawa,K., wagata,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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IQAARQLLSDEQAFLRQKKLADLLHHVSQNITAETREQDPSWFFGLESKFRNKSGYLK
YSCESRIRGYLREVSAYTSMVDEAAQEEYLRVLGSMCQKLKSVGVNGSYFDRGAEASS
RLCTPEGWFSCGGFFDLESCLSKHSINPYGNRESRILFSTWNLDHIIEKKRTVPFTLA
EALQDGREVNWEYFYSLLFTAENIKLYHIACHKKTTHKLECDRSRIYRPQTGSRRKQP
ARKKRPAKKR"

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                                                                                                                                                                                                                   /organism="Mus musculus"
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                                                                                                                                                         'gene="CAD"
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MEDLINE
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Rattus norvegi
complete cds.
AF136598
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Direct Submission
Submitted (23-MAR-1999) Department of Neurology, BST,
Submitted (23-MAR-1999) Department of Neurology, BST,
Pittsburgh University Medical School, 3500 Terrace Str
Pittsburgh, PA 15213, USA
24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1316)
Cao.G., Pei.W., Lan.J., Stetler,R.A., Luo,Y., Nagayama,T.,
Graham,S.H., Yin,X.M., Simon,R.P. and Chen,J.
Caspase-activated DNase/DNA fragmentation factor 40 mediates
apoptotic DNA fragmentation in transient cerebral ischemia and
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                                                                     GTGCTCCCCCAACCCAAATGCGTCAAGTTGCGAGCTCTACACACCTCGTGCAAGTTCGGC 83
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YSCESRIKGYLKEVSAY ISMVDAAAREEYLRVLSSMCHKLKSVQYNGSYDRGABASS
RLCTPEGWFSCQGPEDLESCLSKISINPYGNRESRILFSTWAIDHIIEKKRTVVPPLA
EAJIODGREVWWEYETSLLFTAENLKLVHIACHKKTTHKLQCDRSRIYRPQTGSRRKQP
PRKQPPRKROPTROG
383 C 376 g 273 t
                                                                                                                                                                                                                                                                                                                                                                                                                            /product="caspase-activated deoxyribonuclease"
/protein_id="AAK16646.1"
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/db_xref="GI:13249028"
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PGSRLCMYEDGTEVTDDCFPSLPNDSELLLLTAGETWHGYVSDITRLLSVENEPHAGV
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/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 TATGTGAGTGACATCACACGTCTCCTCAGTGTGTTTAACGAGCCACATGCCGGGGTCATC
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Human DNA sequence from clone
     Eukaryota; Metazoa;
Mammalia; Eutheria;
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     Chordata;
Primates;
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e RP11-205M20 on chromosome
     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RP11-205M20 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   requests: clonerequest@sanger.ac.uk

On Oct 21, 2001 this sequence version replaced gi:15021313.

During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.chori.org/bacpac/home.htm
                                                                                                                                           ValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuPro
                                                                 GluArgGlySerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPhe
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/clone="RP11-205M20"
/clone_lib="RPCI-11.1"
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Direct Submission
Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                       AL355811 142970 bp DNA linear HTG 10-JUL-2001 Homo sapiens chromosome 9 clone RP11-562A11 map pl3.1-21.1, *** SEQUENCING IN PROGRESS ***, 26 unordered pieces.
                                                                                                                                                                                                                    HTG;
                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                    AL355811.4 GI:9863741
                                                                                                                                                                                                                                                         AL355811
                                                                                              Mclay,K
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                                                                                                                                                                                                                                                                                                                                                                                               GAATCTACAAACCCCAGACAAGGTTGAAGAGGAAGTGGCCTGTGTGAAAGCGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGAAGAGAAGTGGACTGGGAATATTTTTATGGCCTGCTTTCTACCTCAGAGAACCTAA
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                                                                                                                 (bases 1 to 142970)
                                                                                                                                                                                                                HTGS_PHASE1;
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                                                                                                                                                                                                                  HTGS_CANCELLED
                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Contact: humquery@sanger_ac.uk
Conter project name: bA552A1.
Center project name: bA552A1.
Summary Statistics
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Sequencing vector: plasmid; L08752; 100% of
Chemistry: Dye-terminator ET-amersham; 18%
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Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39612 39711: gap of 100 bp 11 length 1838 48437; gap of 100 bp 10 length 1838 48437; gap of 100 bp 100 bp 100 length 1838 50511: gap of 100 bp 50612 52986; contig of 2074 bp in length 52987 53086; gap of 100 bp 53087 5956; gap of 100 bp 5367 5956; gap of 100 bp 64910 65009; gap of 100 bp 64910 65009; gap of 100 bp 65010 65095; gap of 100 bp 65010 65005; gap of 100 bp 65010 650000; gap of 100
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4034 4133: gap of 100 bp
4134 8168: contig of 4035 bp in length
8169 8268: gap of 100 bp
8269 14731: contig of 6463 bp in length
14732 14831: gap of 100 bp
14832 18803: contig of 3972 bp in length
18904 18903: gap of 100 bp
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75979: gap of 100 bp 10
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/note="assembly_fragment:00027
fragment_chain:3"
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/note="assembly_fragment:00476"
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CAD/DEF40 nuclease is dispensable for high molecular weight cleavage and stage I chromatin condensation in apoptosis
J. Biol. Chem. 276 (48), 45427-45432 (2001)
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/db_xref="GI-17226274"
/db_xref="GI-17226274"
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RLCLYEDGTELSEAFFRTLPPQTELVLLRPGESWPGCCGDVERFLAALCSRTDAVVEA
ARRILEDERAPRRQRLLADLHNLSGDSAAERRDEDGKWFEGLESRFKNKSYMRYSC
ESRIRSYMKEVSNFISNVHPTARDAYKRILDHADKLKKNUSYFDRTVPEEBAANRL
CTKEGWFEGGGFFDRDGVCPCKHSINPYTNRESRILFSTWNLDHIIEKKRSVVPELAAR
CTKTGGREVNWEYFYGLLFTMNNLKLVHIACHKKTNHNLSCDKTKITKKKRQTHEIS"
345 c 403 g 349 t
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/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="nuclease"
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                                        7.15e-89
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58.30%
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(1-1499)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             556 TATAAAAGGATACTTGACCTGATGTCGGATAAACTGAAATCTGTGAAATATAACGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              496 AGCTACATGAAAGAGGTTAGTAATTTTATTTCAAATGTTCATCCTACAGCGAGAGATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 SerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGlnGluGlu 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436 GAATCTCGTTTTAAGAACAAATCGAGCTATATGCGGTACAGCTGTGAAAGCAGAATACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 GluSerArgPheGlnSerLysSerGlyTyrLeuArgTyrSerCysGluSerArgIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 CTGAGCGGGGACAGCGCGGCCGAGCGCCGGGACGGGAAGTGGTTCGAGGGTCTC
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Danio rerio

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

1. (bases 1 to 1159)
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Danio rerio caspase-activated DNase mRNA,
AF286179 .
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                                                                                                                                                                           and Huang, C.J.
                                         /organism="Danio rerio"
/db_xref="taxon:7955"
25...1026
                                                                                          Location/Qualifiers
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                                                                                                                        (10-JUL-2000) Institute
28, Yen-Chiu-Yuan Road, S
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Section 2, Taipei 115, Taiwan
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                                   243 ProTyrSerAsnArgGluSerArgIleLeuPheSerThrTrpAsnLeuAspHisIleIle
                                                                                                            223 TTpPheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHisSerIleAsn
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                                                                                        TGGTTCTCCTGCCAGGGTGCTTTTGATGAGAACAGCTGCAATTTTCTGCATTCAATAAAC
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                                                                                                                                                                                                                                                                                                       Chemistry: Dye-terminator; 2% of reads
Chemistry: Dye-terminator Big Dye; 97% of reads
Chemistry: Dye-terminator Big Dye; 97% of reads
Consensus quality: 158827 bases at least Q40
Consensus quality: 159096 bases at least Q30
Consensus quality: 159180 bases at least Q20
Insert size: 160716; sum-of-contigs
Insert size: 160716; sum-of-contigs
Insert size: 170984; 0.48 error; agarose-fp
Quality coverage: 10.84x in Q20 bases; sum-of-contigs Quality
coverage: 10.19x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160716 bp
Homo sapiens chromosome 1 clone
PROGRESS ***, in ordered nton-
AL691572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: Web site: htt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 25, 2002 this sequence version replaced gi:21732123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 160716)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL691523
AL691523.5 GI:21955581
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White, S
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                                                                                                                                                                                                                        by the finished sequence as soon as it the accession number will be preserved.
                                                                                                                                                                                                                                                          This sequence will be replaced
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                              vector_side:left
                                                  clone_end:SP6
                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                   /clone="RP13-531C17"
/clone_lib="RPCI-13.3"
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1. .160716
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                                                                note="assembly_fragment:03871"
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            /cell_line="JCR"
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US-09-748-451-2 (1-338) x AL691523
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                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mall:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens cDNA FLJ25547 fis, AKO98413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Kathara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
                                                                                                                                                        Economy, Trade and Industry of Japan; cDNA full insert sequencing Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Hum.
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Sugano, S. and Suzuki
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                                                                                                                                                                                                                               NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing:
                                                                                                                                                                                                                                                                               Fax:81-3-5449-5416)
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insert sequencing: RAB and Helix Research 1
/db_xref="taxon:9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 -----GTCCTCGACGATGCCGAGCTGGTGCTCCTCACCCCAGGCCTGGCAGGGC 134
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13 CGACCTCCTGTAC 1
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/db_xref="GI:31750420"
/db_xref="GI:31750420"
/translation="Membridgling and a protein a
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/note="cloning vector: pME18SFL3"
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76.80%
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Matches:
Conservative:
Mismatches:
Indels:
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Search completed: May 26, 2003, 16:20:42 Job time: 3232 secs

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Title:
Perfect score:
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_FUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_FUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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10 US-9-748-451-4

10 US-9-748-451-3

10 US-10-165-135-3

10 US-10-165-800-11

10 US-10-165-800-15

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10 US-10-165-800-15

10 US-10-165-801-13-6

10 US-10-165-801-13-6
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US-10-165-800-13

US-10-242-943-12

2 US-10-152-647-4
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US-09-935-642-3
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Sequence 12, Appl 1
Sequence 12, Appl 1
Sequence 4, Appl 1
Sequence 4
                                                                                                                                                                                                                                        Sequence 302, Apply Sequence 3, Appli Sequence 155, Appli Sequence 3, Appli Sequence 14, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 15, Appli Sequence 14, App
                                                                                                                                     Sequence 3, Appli
Sequence 1495, Ap
Sequence 11, Appl
Sequence 15, Appl
Sequence 3, Appli
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Sequence 23,
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302, App
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4.2	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.4	4.4	4.4	4 4	4.4	4.4	4.5	4.5	4.6	4.6	4.6	4.6	4.6
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US-09-843-676-217	US-09-050-516-42	US-10-278-547-42	US-10-053-753-2	US-09-853-625B-11	US-09-801-368-370	US-10-197-666A-102	US-09-799-875-17	US-10-197-666A-104	US-09-800-729-206	US-09-987-107-37	US-10-197-666A-48	US-09-925-300-1664	US-09-950-046A-2	US-09-820-843A-58	US-10-003-496-6	US-10-120-687-1	US-10-136-891-2	US-09-963-875-1	US-09-859-888-5	US-09-772-316-2	US-10-118-328-5	us-10-151-193-5	US-10-151-193-6	US-10-097-340-18	US-10-097-340-19
	Sequence 42, Appl		~	Sequence 11, Appl	Sequence 370, App	-	Sequence 17, Appl		Sequence 206, App	Sequence 37, Appl	Sequence 48, Appl	Sequence 1664, Ap	Sequence 2, Appli	õ	e 6,	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli		e 2	Sequence 5, Appli	Sequence 5, Appli	Sequence 6, Appli	Sequence 18, Appl	Sequence 19, Appl

ALIGNMENTS

RESULT 1 US-09-748-451-2 ; Sequence 2, Application US/09748451 ; Patent No. US20010011078A1

APPLICANT: WANG, XIRODONG
APPLICANT: LIU, XUESONG
ITILE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN APOPTOSIS
FILE REFERENCE: UTSD:546USD1
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/061,702
PRIOR APPLICATION NUMBER: 09/061,702
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
SEQ ID NO 2
SEQ ID NO 3
LENGTH: 338
LENGTH: 338
ORGANISM: Homo sapiens Q ρ 밁 밁 Qy 망 밁 Query Match 100.0%; Score 1789; DB 10; Length 338; Best Local Similarity 100.0%; Pred. No. 8.3e-158; Matches 338; Conservative 0; Mismatches 0; Indels 0; 121 DLLHNYSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTYGA 180 181 181 EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS 240 241 INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK 300 121 DLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGA 180 61 61 PSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLA 120 1 MIQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF 60 EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGFFDMDSCLSRHS PSVPDNAELVLLTIGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLA 120 MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF 60 0; Gaps

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US-10-165-800-13
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                Sequence 12, Application US/10242943 Publication No. US20030087412A1 GENERAL INFORMATION:
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LENGTH: 76
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TITLE OF INVENTION:
TITLE OF INVENTION:
ITLE OF INVENTION:
ILE REFERENCE: 35800
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Publication No.
   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/185,946 PRIOR FILING DATE: 2000-02-29
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                                                                                                                                                                                                                                                                                                                                                           PERATURE:
OTHER INFORMATION: Consensus sequence for the -165-800-13
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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Nandabalan, Krishnan
                                                                                                                                             ALEQGEKW 76
                                                                                                                                                                                                               RNVRK-GVAASSLEELLSKVLDKLKLPDSLEPVTLVLEEDGTEVEDEEYFRTLPNNTELV 68
                                                                                                                                                                                                                                RSPRKFGVAGRSCQEVLRKGCLRFQLPE--RGSRLCLYEDGTEL-TEDYFPSVPDNAELV 70
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Meyers, Rachel E.
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44.1%; Pred. No. 0.0023;
Live 12; Mismatches 22; Indels
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                                                                             ; TYPE: PRT
; ORGANISM: Mus
US-10-152-647-4
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US-10-152-647-4
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: TYPE: PRT

: ORGANISM: Homo sapiens

US-10-242-943-12
                                                                                                                                                          SOFTWARE: PatentIn
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                     Query Match
Best Local (
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   Matches
                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
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Best Local Similarity 20.8%;
                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/152,647
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US/09/610,401
PRIOR FILING DATE: 2000-07-05
                                                                                                                                                                                                                                                                                      APPLICANT: SHIBATA, Takehiko
TITLE OF INVENTION: Antibody against cleavage product of vimentin
FILE REFERENCE: 522.1004
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                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/09/167,206 PRIOR FILING DATE: 1998-10-06
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                                                                                                                                      LENGTH: 466
                   Local
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   63;
                   Similarity
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   Conservative
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20.1%;
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Score 99; DB 12; Length 46;
Pred. No. 0.69;
7; Mismatches 113; Indels
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Pred. No. 0.69;
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US-10-043-487-302
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US-10-043-487-302
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SEQ ID NO 302
LENGTH: 405
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Publication No. US20
GENERAL INFORMATION:
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TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptic
TITLE OF INVENTION: Mammalian polypeptides
FILE REFERENCE: B4778A
CURRENT APPLICATION NUMBER: US/10/043,487
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
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APPLICANT: Pierre, LE
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Local Similarity 20.8%;
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                               383 IKTVETRDGQVIN 395
                                                                                    273 VEAIKEQDGREVD 285
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o. US20030055220A1
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TYPE: PRT

ORGANISM: Homo sapiens

US-09-935-642-3
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US-09-935-642-3
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US-09-923-779-155
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CURRENT APPLICATION NUMBER: US/09/935,642
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: PCT/GB97/02394
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR APPLICATION NUMBER: PCT/GB9618600.2
PRIOR APPLICATION NUMBER: PCT/GB9618600.2
PRIOR APPLICATION NUMBER: PCT/GB9618600.2
PRIOR APPLICATION NUMBER: PCT/GB9618600.2
PRIOR FILING DATE: 1996-09-06
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Publication No. US20030044795A1
GENERAL INFORMATION:
APPLICANT: BYRJALSEN, Inger
APPLICANT: LARSEN, Peter
APPLICANT: LARSEN, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                Sequence 155, Application US/09923779 Patent No. US20020076721A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 65; Conserv
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 155
                                                                        APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.53
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
CURRENT FILING DATE: 2001-08-06
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TITLE OF INVENTION: Biochemical Markers for the Human
TITLE OF INVENTION: Endometrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
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US-10-152-647-3
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/152,647
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US/09/610,401
PRIOR FILING DATE: 2000-07-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHIBATA, Takehiko
TITLE OF INVENTION: Antibody against cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Vel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 522.1004
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TYPE: PRT
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RGANISM: Homo sapiens
)-152-647-3
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                                                                                                                                                         87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141
                                                                                                                                                                                                                                      27 QEVLRKGCLREQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86
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                                      YKSKFADLSEAANRNNDALRQAKQESTEYRRQVQSLTCEVDALKGTNESLERQMREMEEN
YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC 226
                                                                                                                                                                                               EDIMR----LREKLQEE-----MLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEI- 231
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SEQ ID NO 14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: No. US20030092116A1el Nucleic Acid Sequences Encoding TITLE OF INVENTION: Adenylate Kinase, Phospholipid Scramblase-Like, DNA TITLE OF INVENTION: Fragmentation Factor-Like, Phosphatidylserine Synthase-Like, TITLE OF INVENTION: and ATPase-Like Molecules and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/165,800 CURRENT FILING DATE: 2002-06-07
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/781,677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-02-29
APPLICATION NUMBER: 09/795,038
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                                                                                                                103 EQGQSWSPKSGMLSYGLGREKPKHSKDIARITFDVYKQNPRDLFGSLNVKATFYGLYSMS 162
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                                      CDFQGVGPKRVLRELLRGTSSQL---
                                                                         CDEQAPORORLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIR 165
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Kapeller-Libermann, Rosana
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25.8%;
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                                                                                                                                                                                                                                                                       Score 91; DB 9;
Pred. No. 1.4;
21; Mismatches
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                                      -QGLGHMLLGISSTLRHVVEGADR 208
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ORGANISM: Homo sapiens
US-09-748-451-4
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US-09-748-451-4
; ORGANISM: Rattus norvegicus US-10-086-135-3
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US-10-086-135-3
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APPLICANT: LIU, XUESONG
TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN APOPTOSIS
FILE REFERENCE: UTSD-546USD1
CURRENT APPLICATION NUMBER: US/09/748,451
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION UNDER: 09/061,702
PRIOR APPLICATION UNDER: 09/061,702
PRIOR APPLICATION UNDER: 09/061,702
PRIOR APPLICATION UNDER: 09/061,702
PRIOR PILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATCENTIN VOI. 2.1
EQ ID NO 4
EXPERCISE 19831
                                                                                                                        CURRENT APPLICATION NUMBER: US/10/086,135

CURRENT FILING DATE: 2002-02-26

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/366,448

PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-03

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/095,199

PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-03

NUMBER OF SEQ ID NOS: 35

SOFTMARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PANCREATIC AND OVARIAN POLYPEPTIDE TITLE OF INVENTION: ZSIG58
FILE REFERENCE: 98-24
CURRENT APPLICATION:
                                                       LENGTH: 45
                                                                                                        ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 YFYGLLFTSENLKLYHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPYRKRQ 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 EVDAVDTGMSRET-----SSDVALAS----HIL-----TALREKQAPE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 QSCATV-QRLQHTLQQVLDQREEVRQSKQLLQLYLQALEKEGSLLSKQE---ESKAAFGE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 SYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFD- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 DSGAGL-----KWKNVARELK------EDLSSIILLSEEDLQMLVDAPCSDLAQELR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 PQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 IVDDDDYFLCLPSNTKFVALASNEKW------AYNNSDGGTAWISQESFDVDET 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 EL-TEDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQA 112
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                                                                              457
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Similarity 22.2%;
78; Conservative 4
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; Pred. No. 3.7;
49; Mismatches 146; Indels 78;
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US-09-925-300-1495
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1495
LENGTH: 366
TYPE: PRT
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5.0%; Score 89; DB 9; Length 457
Best Local Similarity 21.8%; Pred. No. 5.7;
Matches 60; Conservative 40; Mismatches 71; Indels
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION UNMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
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                                                                                                                                                                                                                     152 DSGAGLKWKNVARQLKEDLSSIILLSEEDLQMLVDAPCSDLAQE------LRQSCATV 203
                                                                                                                                                                                                                                                                                                                               104 IVDDDDYFLCLPSNTKFVALASNEKW------AYNNSDGGTAWISQESFDVDET 151
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246 ---ESKAAFGEEVDAVDTGISRET-----SSDVALAS----HIL-----TAL
                                                   222 GWFSCQGPFD-----MDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAI 276
                                                                                                             204 QRLQHTLQQVLD-----
                                                                                                                                                              163 -RIRSYLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPE 221
                                                                                                                                                                                                                                                                            109 DEQAPQRQRLLADLLHNVSQNIAAETRAE-----DPPWFEGLESRFQSKSGYLRYSCES- 162
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22.4%; Pred. No.
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50; Mismatches 131; Indels 100;
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SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/165,800
CURRENT FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 09/790,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ
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                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-02-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER:
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                                   162 --- SRIRSY 167
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211 QQKGRLHSY 219
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                                                                                                                                                                                                                     $5
                                                                                                                                                                             73 TLGQAW----QGYVS------DIRRFLSAFHEPQ-----VGLIQAAQQL 106
                                                                                                                                                                                                                                                     14 RSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTEL-TEDYFPSVPDNAELVLL
                                                                                                       LCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCE----
                                                                                                                                           QSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPRDLFGSLNVKATFYGLYSM 162
                                                                       SCDFQGLGPKKVLRELLRWTSTLL
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Pred. No. 3.5;
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                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local
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LENGTH: 219
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                                                                      APPLICANT: COLLINS, JAMES E.
APPLICANT: FRABERG, Kay S.
APPLICANT: ROSSOW, Kurt D.
TITLE OF INVENTION: PROCISIE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 110.01250101
CURRENT APPLICATION NUMBER: US/10/203,224
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: PCT/US01/04351
PRIOR FILING DATE: 2001-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 35800/247838
CURRENT APPLICATION NUMBER: US/10/165,800
CURRENT FILING DATE: 2002-06-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/790,838 FILING DATE: 2001-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/185,609
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                                                                                                                                                                                                                                                                                                                                                                73 TLGQAW 78
                                                                                                                                                                                                                                                                                                                                                                                                   44 RSSRR-GVMASSLQELISKTLDALVIATGLVTLVLEEDGTVVDTEEFFQTLGDNTHFMIL
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RESULT 16
US-10-143-849-2
US-10-143-849-2
Sequence 2, Application US/10143849
Sequence 2, Application US/10143849
Sequence 2, Application US/10143849
GENERAL INFORMATION:
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/193,220
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/206,624
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/215,373
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 60/260,041
PRIOR APPLICATION NUMBER: 60/260,041
PRIOR APPLICATION NUMBER: 60/260,041
PRIOR PILING DATE: 2001-01-05
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Matches
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LENGTH: 1458
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NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
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                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/143,849
FILING DATE: 14-May-2002
CLASSIFICATION: CUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Genetic control of flowering NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Coupland, George M. Putterill, Joanna J
                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/516,191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 IQAAQQLLCDEQAPQRQRLLADLLHNVSQNIAAETRA------EDPPWFEGL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 RLRSMQYNGSYFDR-----GAKGGSRLCTPEGWFSCQGPF-----DMDSCLSRHSIN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 ---ESRFQSKSGY------LRYSCESRIRSYLREVSSYPSTVGAEAQEEFLRVLG-SMCQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            553 IEAGRQLV-----PNRDRILAALAYHMKAQNASEYYASAAAILMDSCACIDHDPEWYEDL 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  764 PLLPTCKDINMYKVACNVLLSKFIVGPPGSGKTTWLLGQVQDDDVIYTP 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 GLLETSENLKLVHIVCH-------KKTTHKLN--CDPSRIYKP 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        715 PPRTVIMKVGNKTTALDPGRYQSRRGLVAVKRGIA------GNEVDLSDGDYQVV 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              666 -----LFHSHFHQHCPVTLSCGHHAGSRECS-----QCQSPVGAGRSPLDAVLKQIPYK 714
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                                                                                                                                                                                                                                                                                                                                                       CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/945,056
FILING DATE: <Unknown>
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Pred. No. 59;
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TOPOLOGY: Il near
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-143-849-2
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US-10-051-311A-2
Sequence 2, Application US/10051311A
Patent No. US20020164620A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim International GmbH
TITILE OF INVENTION: Method for identifying compounds that modulate sister
TITILE OF INVENTION: Chromatid separation
                                                                                                                                                                                                                                                                                                   ; SEQ ID NO 2;
LENGTH: 2120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-051-311A-2
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Matches
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PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/297,440
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEO ID NOS: 13
SOFTWARE: Patentin Ver: 2.1
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CURRENT FILING DATE: 2002-06-20
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CURRENT ADDITIONTON TOTAL CONTROL OF THE CONTROL OF T
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                                                                                                                                                                                                                        Local
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NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 EKIMIDPEKRLYVDQEEGEEGDKDAKEVASWLFPNSDKNNNNQNNGLLFSDEYLNLVDYN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 GGSRLCTPEGWFSCQGPFDMDSCLSR-HSINPYSNRESRI--,----LFSTWNLDHIIE 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 SGYLRYSCESRIRSYLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 SSMDYKFTGEYSQHQQNCS-----VPQT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 ----HIVCHKKTTHKLNCDPSRIYKPQT 326
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                                                                                                197 RAVAAHQLFDASGHGLNEADADFLDDLLSRHVIRALVGERGSSSGLLSPQRALCLLE--- 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 SAYLCMSCDAQVHSANRVAS-----RHKRVRVCES-CERAPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 -- AFLCEADDASLC-----TACDSEVHSANPLARRHQRVPILPISGNSFSSMTTTHHQS 123
                                             54 ELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFL-SAFHEPQVGLIQAAQQL----- 106
                                                                                                                                                11 RALRSPRKFGVAGRSCQE------VLRKGCLRFQLPERGS-----RLCLYEDGT 53
                                                                                                                                                                                                   66;
                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                4.6%; Score 83; DB 9; Length 2120;
18.8%; Pred. No. 1.7e+O2;
ative 52; Mismatches 130; Indels 104; Gaps
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-LTL-----EHCRRFCWSRHHDKAISAVEKAHSYLRNTNL 287
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                                                                                                                                                                                                                                                   Length 2120;
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RESULT 19
US-10-097-340-23
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; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Wherein Xaa may be any one of Leu
US-09-867-550-1316
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     Sequence 23 Application US/10097340 Publication No. US20030087250A1 GENERAL INFORMATION:
APPLICANT: John MONAHAN
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SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 1316
LENGTH: 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells
TITLE OF INVENTION: Thereby
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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Cent No. US20020082206A1
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Pred. No. 11;
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; LENGTH: 633
; TYPE: PRT
; ORGANISM: Homo sapiens
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APPLICANT:
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SOFTWARE: FastSEQ for Windows Version
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TITLE OF INVENTION: Assessment,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/324,967 FILING DATE: 2001/09/26
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393
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                                                                                                       RTIIPTLVEAIKEQDGREVD
                                                                                                                                           FGRRVVT----FSCCRMPPSHELDHQRLLEYLKYTLDQYVENDYTIVYFHYGLN---SRN
                                                                                                                                                                                                                                                     ----EFLR----VLGSMCQRLRSMQYNGS----
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Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
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Robert C. BAST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sebastian HOERSCH
Shubhangi KAMATKAR
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Pred. No. 3
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SEQ ID NO 19
LENGTH: 718
TYPE: PRT
ORGANISM: Homo sapiens
0-097-340-19
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4.6%; Score 82.5; DB 9; Length 718;
Best Local Similarity 20.1%; Pred. No. 42;
Matches 73; Conservative 48; Mismatches 116; Indels 127; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR FILING DATE: 2001-03-14
OR APPLICATION NUMBER: 60/325,149
OR RETLING DATE: 2001-09-26
OR APPLICATION NUMBER: 60/276,026
OR FILING DATE: 2001-03-14
OR APPLICATION NUMBER: 60/324,967
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NUT FILING DATE: 2002-03-14
APPLICATION NUMBER: 60/276,025
FILING DATE: 2001-03-14
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FILING DATE: 2001-08-10
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                                                                                                                                                                                170 HARVPPAIVOMLLVLOGVHESRGVTEDYLR--LETLVQ---KVVSPYLGTYGLHSSEGPF 224
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                                                                                        225 THSCILELQRDKAAAAAVLGAVRKRPSVVPMAGQDPALSTSHPFYDVARHGILQVAGDDR 284
                                                                                                                                   185 -----EFLR------VLGSMCQRLRSMQYNGS-----YFDRGAKG------ 213
                                                                                                                                                                                                                              135 RAEDPP-----WFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGAEAQE--- 184
                                                                                                                                                                                                                                                                           124 SDVLPMLQAIFYPVQGKEPSVRQLA-------LHFRNAITLSVKLEDALARA 169
285 FGRRVVT----FSCCRMPPSHELDHQRLLEYLKYTLDQYVENDYTIVYFHYGLN---SRN 337
                                          214 -GSRLCTPEGWFSC-----QGPFDMDSCLS--RHSINPYSNRESRILFSTWNLDHIIEKK 265
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                                                                                                                                                                                                                                                                                                                                                                                                               37 FQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLL------TLGQAWQGYV 82
                                                                                                                                                                                                                                                                                                                      83 SDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLADLLH-----NVS-QNIAAET 134
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Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
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No. US20030087250A1
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Robert C. BAST, Jr.
Karen LU
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S-223423-4
US-08-847-900-3
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US-09-069-023-32
US-08-157-005-3
US-08-157-07-27
US-08-286-819A-27
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MLQKPKSVKLRALRSPRKPGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF 	ch l Similarity 338; Conser	uence 2, Application US/090 ent No. 6165737 MERAL THYORMATION: APPLICANT: L14, Xuesong TITLE OF INVENTION: DNA FR TITLE OF INVENTION: DNA FR TITLE OF INVENTION: APPLICANT: L14, Xuesong TITLE OF INVENTION: DNA FR TITLE OF INVENTION: APPLICATION OF SEQUENCES: 21 CORRESSONDENCE ADDRESS: ADDRESSEE: Arnold, White STRATE: TX COUNTRY: USA ZIP: 77210-4433 COMPUTER: ERADABLE FORM: WEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati OPERATING SYSTEM: PC-DOS SOFTWARE: PATENTION NUMBER: USA CURRENT APPLICATION NATA: APPLICATION UNMERE: PC-DOS SOFTWARE: MCMIllian, Nabeela RESISTRATION UNMERE: PC-DOS TILING DATE: CONCUTENTION LANSIFICATION INFORMATION: NAME: MCMIllian, Nabeela REFERBACE/DOCKET NUMBER: USA REFERBACE/DOCKET NUMBER: USA TELECOMMUNICATION INFORMATION TELECOMMUNICATION ON THE STRANDED NESS TELECOMMUNICATION ON THE STRANDED NESS TELECOMMUNICATION ON THE STRANDED NESS TOPOLOGY: 11near TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: TOPOLOGY: 11near		
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SEQ ID NO 4
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Best Local
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CURRENT FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: JP 11-193235
PRIOR FILING DATE: 1999-07-07
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TITLE OF INVENTION: Antibody against cleavage product of vimentin
FILE REFERENCE: 522.1004
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                                                                                                                           VEAIKEODGREVD 285
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                                                                                                                                                                                                           QGPFDMDSCLSRHSINPYSNRESRI----LFSTWNLDHI---
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                                                                                                                                                                                                                                                                                                                                  YKSKFADLSEAANRNNDALRQAKQESNEYRRQVQSLTCEVDALKGTNESLERQMREMEEN 350
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; SEQ ID NO 18
; LENGTH: 219
; TYPE: PRT
; ORGANISM: MUS mUSCU
US-09-069-023-18
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  Query Match 5.3
Best Local Similarity 25.8
Matches 46; Conservative
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Best Local Similarity 20.8%; Pred. No. 0.088;
Matches 65; Conservative 46; Mismatches 112; Indels
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                                                                                                                                                                                                                                                                APPLICANT: Nunez, Gabriel
APPLICANT: Inchara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS
FILE REFERENCE: UM-03333
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                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SHIBATA, Takehiko
TITLE OF INVENTION: Antibody against cleavage product of
FILE REFERENCE: 522.1004
CURRENT APPLICATION NUMBER: US/09/610,401
CURRENT FILING DATE: 2000-07-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 11-193235
PRIOR FILING DATE: 1999-07-07
NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 466
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 VEAIKEQDGREVD :: :: :||: ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 FAVEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232. AFLKKLHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 YKSKFADLSEAANRNNDALRQAKQESTEYRRQVQSLTCEVDALKGTNESLERQMREMEEN 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 EDIMR---LREKLQEE----MLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGPFDMDSCLSRHSINPYSNRESRIL-----FST-----WNLDHI----IEKKRTIIPTL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KMALDIEIATYRKLL---EGEESRISLPLPNFSSLNLRETNLDSLPLVDTHSKRTF---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKTVETRDGQVIN
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                                                                                                     musculus
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5.1%; Score 91; DB
25.8%; Pred. No. 0.1;
tive 21; Mismatches
                                                                                                                                                                                      2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456
                                          BB
                                          4.
                                        Length 219;
                                                                                                                                                                                                                                                                                          IDENTIFYING APOPTOSIS AND ACTIVATORS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (512)474-7577
NFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quence 4, Application US/09061702
tent No. 6165737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
TYPE: amino acid
TOPOLOGY: line
(OLECTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MGMILLIAN, NADGELA R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, Wh.
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN ITLE OF INVENTION: APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: Concur
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ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                         POCGT
  173 SYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFD- 231
                                                                                                          113 PQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 CDFQGVGPKRVLRELLRGTSSQL-------QGLGHMLLGISSTLRHVVEGADR 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 CDEQAPQRORLLADILHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIR 165
                                                                  117 DSGAGL-----KWKNVARELK-----EDLSSIILLSEEDLQMLVDAPCSDLAQELR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 EQGQSWSPKSGMLSYGLGREKPKHSKDIARITFDVYKQNPRDLFGSLNVKATFYGLYSMS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 RTVRK-GLTAASIQELLDK-VLETILLRGVLTLVLEEDGTAVDSEDFFQLLEDDTCLMVL 102
                                                                                                                                                     69 IVDDDDYFLCLPSNTKFVALASNEKW------AYNNSDGGTAWISQESFDVDET 116
                                                                                                                                                                                                 54 EL-TEDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQA 112
                                                                                                                                                                                                                                            10 PESGEIRTLKPCLLRRNYSREQHGVAA-SCLEDLRSKACDILAIDKSLTPVTLVLAEDGT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 TLGQAW---QGYVS------DIRRFLSAFHEPQ------VGLIQAAQQLL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 RSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTEL-TEDYFPSVPDNAELVLL 72
                                                                                                                                                                                                                                                                                    5 PKSVKLRALR-----SPRKFGVAGRSCOEVLR-KGC--LRFQLPERGSRLCLYEDGT 53
                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                             5.0%; Score 89; DB 4; Length 331; ilarity 22.2%; Pred. No. 0.38; Conservative 49; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Concurrently Herewith
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                                                                                                                                                                                                                                                                                                                                78; Gaps
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Best Local !
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APPLICANT: Shah, purd
TITLE OF INVENTION: NOVEL NE
TITLE OF INVENTION: PROTEIN
NUMBER OF SECURIORS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOSTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,900
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 442368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
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CITY: Palo Alto
                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
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150 ------QSKSGYLR------ 177
                                                                                                        101 QAAQQLLCDEQAPQRQ-RLLADLLHNVSQNIAAETR--AEDPPWFE------GLESRF- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 YFYGLLFTSENLKLVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 EVDAVDTGMSRET-----SSDVALAS----HIL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 QSCATV-QRLQHTLQQVLDQREEVRQSKQLLQLYLQALEKEGSLLSKQE---ESKAAFGE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 ----LSLSSQDLELVTKEDPKALAVALNWDIKKTETVQEACERELALRLQQ 299
                                                                                                                                                                               44 SRICLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQ---VGLI 100
                                                                  50 VAPQQTMCSRDARTKQLRQLLEKVQNMSQSIEVLDRRTQRDLQYVEKMENQMKGLESKFR 109
                                                                                                                                                                                                                                            60;
                                                                                                                                                   9 SLLVLLVMGTELTQ----VLPTNPE-----ESWQVY-----SSAQDSEGRCICTV 49
                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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3174 Porter Drive
                                                                                                                                                                                                                                         5.0%; Score 89; DB 2; Length 457; llarity 21.8%; Pred. No. 0.62; Conservative 40; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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TER: 36,749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOVEL NEURONAL EXTRACELLULAR MATRIX
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                                                                                                                                                                                                                                       71; Indels 104;
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Larson, Marina

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                 ZIP: 80443-5270
COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                            SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                               COMPUTER: Lbn COMPUTER: MS DO OPERATING SYSTEM: MS DO OPERATING SYSTEM: MS DO OPERATION DATA:
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ID NO:4:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                 ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US
FILING DATE: 03-31-1989
                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                STREET: PO BO
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                 CLASSIFICATION:
                                                                                                                                                              COUNTRY: USA
ZIP: 80443-5270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             913 KVLPQGWKGSPAIFQYTMRQVLEPFRKANPDVIIVQYMDDILI---ASDRTDLEHDKVVL 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                861 PHPAGLAKKRRITVLDVGDAYFSIP-----LYEDFRQYTAFTLPSV-NNAEPGKRYIY 912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 PRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAE----LVL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
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                                                                                                                                                                                                                                 PO Box
                                                                                                                                                                                                                                                                                                                                               Huq, A.H.M. Mahbubul
Chopra, Vikramjit Singh
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                                                                                                                                                                                                                                                                                                                                                                                               Hayden. Michael R.
                                                                                                            IBM Compatible
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                                                                                                                                                                                                                                                                                                 Huntington's Disease
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                                                                                              MS DOS 5.0
                                                                                                                                                                                                                                                                                                                                 Michael
                                              US/09/085,199E
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Pred. No. 1:
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                                                                           US-09-069-023-32
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US-09-069-023-32
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                                                                                                           SEQ ID NO 32
LENGTH: 331
TYPE: PRT
 Query Match 4.9%; Score 87; DB 4; Length 331; Best Local Similarity 22.4%; Pred. No. 0.62; Matches 81; Conservative 50; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27
                                                                                                                                                                                                                                TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS FILE REFERENCE: UM-03333
                                                                                                                                                                SOFTWARE: PatentIn Ver.
                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                   APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (970) 668-20 INFORMATION FOR SEQ ID NO:
                                                                                        ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION:
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HYPOTHETICAL: no
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NO. 6348573
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72; Conserv
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Pred. No. 1.7;
47; Mismatches
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1.7;
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   100;
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     Gaps
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APPLICATION NUMBER: EP 91201398.4 FILING DATE: 06-JUN-1991 PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: EP 92200781.0 FILING DATE: 18-MAR-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/NL92/00096 FILING DATE: 05-JUN-1992 ATTORNEY/AGENT INFORMATION: NAME: MOTAN, Thomas F REGISTRATION NUMBER: 16,579 REFERENCE/DOCKET NUMBER: 44819 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 977-9550	ZIF: 10112 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: TBM PC compatible SOFTWARE: Patentin Release #1.24 CURESMY APPLICATION UNDER: US/08/157,005 FILING DATE: 26-NOV-1993 CLASSIFICATION: 424 PRIOR APPLICATION: 424 PRIOR APPLICATION: 424	APPLICANT: Moorman, Robertus J APPLICANT: Meulenberg, Johanna J TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE, TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza CITY: New York STATE: New York COUNTRY: USA	RESULT 10 US-08-157-005-3 ; Sequence 3, Application US/08157005 ; Patent No. 5620691 ; GENERAL INFORMATION: ; GENERAL INFORMATION: ; APPLICANT: Wensvoort, Gert ; APPLICANT: Terpstra, Catharinus ; APPLICANT: Pol, Johannes M		222 GWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAI 276	Db 117 DSGAGILWRVARQLKEDIJSSIILIJSEEDIJQHIJVDAAPCSDLAQELRQSCATV 168 OY 163 -RIRSVLREVSSYPSTVGAEAQEEFLRVIGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPE 221 ::	Qy 5 PKSVKLRALRSPRKFGVAGRSCQEVLR-KGCLRFQLPERGSRLCLYEDGT 53 : :: : :
							
COPEMATING SEGIEM: WINDOWS SOFTWARE: ASCII CURRENT APPLICATION DATA: COURRENT APPLICATION NUMBER: US/08/747,863 FILING DATE: PRIOR APPLICATION LOTA: APPLICATION NUMBER: US 08/157,005 FILING DATE: 26 NOV-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: EP 91201398.4 FILING DATE: 06 -JUN-191 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION UMBER: EP 92200781.0 FILING DATE: 18 -MAR-1992 FILING DATE: 18 -MAR-1992	DENCE ADDRES EE: Trask, E525 South 525 South Salt Lake C1 Utah UTAh 1111 VSA 1111 VSA 1111 VSA 1111 VSA 1111 VSA 1111 VSA 111 VSA 1111 VSA 111 VSA 1111 VSA 1111 VSA 1111 VSA 1111 VSA 1111 VSA 1111 VSA 111 VSA 1111 VSA 111 VSA 1111 VSA 1111 VSA 1111 VSA 1111 VSA 1111 VSA 1111 VSA 111 VSA 1111 VSA 111 VSA 1111 VSA 1111 VSA 1111 VSA 1111 VSA 1111 VSA 1111 VSA 111 VSA 1111 VSA 111 VSA 11		TSENLKLYHIVCH	Db 671LFHSHFHQHCXVTLSCGHNGSKECSQCQSPVGAGRSPLDAVLKQIPYK 719 Qy 243 PYSNRESRILESTWNLDHIEKKRTIIPTLVEAIKEQDGREVDWEYEYGLLF 294	Db 558 IEAGROLVPURDRILAZIHUKAQNASEYYASAAAILMDSCACIDHDEWYEDL 612 QY 146ESREQSKSGYLRYSCESRIRSYLREVSSYPSTVGAEAQEEFLRVLG-SMCQ 195	Query Match 4.8%; Score 86.5; DB 1; Length 1463; Best Local Similarity 22.1%; Pred. No. 6.8; Matches 63; Conservative 41; Mismatches 96; Indels 85; Gaps 15; Matches 10: IQAAQQILCDEQAPORORIADILHNYSQNIAAETRAEDPPWFEGL 145 Oy 10: IQAAQQILCDEQAPORORIADILHNYSQNIAAETRA	; TELEFAX: (212) 315-1931 ; TELEX: 422533 COOP UI ; INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1463 amino acids ; TYPE: amino acid ; TYPE: TYPE: Amino acids ; NOLECULE TYPE: protein US-08-157-005-3

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US-09-565-864-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09565864 Patent No. 6455245 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (801) 531-916 INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 532-1922
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ATTORNEY/AGENT INFORMATION:
NAME: Turner, Allen C.
REGISTRATION NUMBER: 33041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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Local Similarity 22.1%; Pred. No. 6.8;
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                                                                                 ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                   CURRENT APPLICATION DATA:
PRIOR
                                                                                                                                                                                                                                                                                                                                               TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wensvoort,
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 IQAAQQLLCDEQAPQRQRLLADLLHNVSQNIAAETRA-------EDPPWFEGL 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
           APPLICATION NUMBER: US/09/565,864 FILING DATE: 05-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                 CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPRTVIMKVGNKTTALDPGRYQSRRGLVAVKRGI-----AGNEVDLSDXDYQ-VVPLLP 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYSNRESRILFSTWNLD------HIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLF 294
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                                                                                                                                                                                                COUNTRY: USA
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1463 amino acids
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                                                                                                                                                                                                                                                                                                                           Meulenberg, Johanna J
INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
                                                                                                                                                                                                                                                                                                                                                                                                                 Terpstra, Catharinus
                                                                                                                                                                                                                                                                                                                                                                               Moorman, Robertus J
                                                                                                                                                                                                                                                                                                                                                                                                Pol, Johannes M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96;
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                                                 ; ORGANISM: Homo US-09-069-023-12
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                                                                                                                      SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                           Sequence
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Best Local 9
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                                                                                  LENGTH: 2:
TYPE: PRT
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SEQUENCE DESCRIPTION: SEQ ID NO: US-09-565-864-3
                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6348573
GENERAL INFORMATION:
  Query Match
Best Local Similarity
                                                                                                                                                                                                                      APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REPERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 422523 COOP UI INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/NL92/00096 FILING DATE: 05-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 92200781.0 FILING DATE: 18-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/157,005 FILING DATE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09069023A
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22.1%; Pred. No. 6.
4.8%;
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Pred.
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    NO ;
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    DB 4;
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                       Length 219;
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RESULT 14
US-08-286-819A-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                  TELEX: (703) 413-3000
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 2296 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1/55
STREET: 1/55
CITY: Arlington
TWATE: Virginia
TW.S.A.
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
MOLECULE TYPE:
3-286-819A-27
                                                                                                                                                  NAME: Oblon, No. 5871910man REGISTRATION NUMBER: 24,618 REFERENCE/DOCKET NUMBER: 660 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Oblon, No. 5871910man F.
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 29-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
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                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/286,819A FILING DATE: 05-AUG-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 10-AU
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 31-OC
                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 RSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTEL-TEDYFPSVPDNAELVLL 72
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                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COURVALIN,
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                                                                                                                                                                                                                                                 31-OCT-1990
N: 435
                                                                                                                                                                                                                                                                                                                                                                                                   10-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYPEPTIDES IMPLICATED IN THE EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                PCT/FR/91/00855
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                                                                                                                                                                                        660-060-0 PCT
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Best Local Similarity
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                    TELEFAX: (703) 413-22:
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 0/
APPLICATION NUMBER: US 0/
FILTING DATE: 05-AUG 1994
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 29-OCT-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 10-AUG-
PRIOR APPLICATION DATA:
  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1755 S. CITY: Arlington STATE: Virginia
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                                                                    TELEPHONE:
                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                       (703) 413-3000
                                                                                                                                                                                                                                 29-OCT-1991
                                                                                                                                                                                                                                                                                   10-AUG-1992
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                                                      413-2220
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,35
FILING DATE:
TELECOMMUNICATION INFORMATION:
                                                                       ATTORNEY/AGENT INFORMATION: NAME: Oblon, No. 6013508man F.
                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/174,682
PRICE DATE: 28-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1367 WMYWKERKSFSTLIAPKNOLIINFYLNFKECLTSHRIRP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 -- FDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEK 264
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1755 S. Jefferson Davis Highway, Suite 400
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                                                                                                                                               FR 9013579
                                                                                                                                                                                                                                                                                         US 07/917,146
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Pred. No. 17;
17; Mismatches
                              660-060-0 PCT
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US-08-980-357-27
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Best Local
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Best Local (
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                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: GB 9 FILING DATE: 02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/GB95/02561 FILING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/OFILING DATE: 20-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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les 33; Conserv
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                               Local Similarity
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   36
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                            SGYLRYSCESRIRSYLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAK 212
 SAYLCMSCDAQVHSANRVAS:
                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                           Ms Mary J Wilson
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8th Floor, 1100 No. 6077994th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States of America
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                                                               Conservative
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22.68;
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                                                            Score 84.5; DE
Pred. No. 1.4;
26; Mismatches
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Pred. No. 17;
17; Mismatches
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-RHKRVRVCES-CERAPA-
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71
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; SEQ ID NO 31
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-069-023-31
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Best Local Similarity
Matches 23; Conserva
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Patent No. 6348573
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                                  Query Match
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TYPE: PRT
ORGANISM: Mus (
                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS FILE REFERENCE: UM-03333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                           SOFTWARE: PatentIn
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APPLICANT: Koseki, Takeyoshi
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APPLICANT: KOSeki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
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o. 634857:
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                                                                                                                                                                                                                                                                                                                   Nunez, Gabriel
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 Conservative
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                                                                                                                                                           Ver.
                  4.7%; Score 83.5;
28.8%; Pred. No. 0.
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36.4%; Pred. No. 0.68;
tive 11; Mismatches
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 19; Mismatches
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                                  DB 4;
 35;
                                Length 239;
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CURRENT APPLICATION NUMBER: US/09/413,814
CORRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 2618
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-413-814-28
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US-09-069-023-20
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GENERAL IMPORMATION:

APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.7%; Score 83.5; DB 4; Length 2618; Best Local Similarity 23.0%; Pred. No. 35; Matches 54; Conservative 25; Mismatches 89; Indels 67
                                                                                                                                                                                                                                               Sequence 20, Application US/09069023A Patent No. 6348573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cino, Paul M
APPLICANT: Cino, Paul M
APPLICANT: Coldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Mueller, Joachim
APPLICANT: Mueller, Joachim
APPLICANT: Reschenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
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APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Beyer, Stefan
PPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
                                                                                                                                                                                                                                                                                                                                                                                                                                        2214 LALARHLARKYRATLILAGRRGAP---ARELWHQAPAEFVPVAAAIAQMEECGAR 2265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2161 MGAAPGPEEIALRGTSRWELGYEPVEGGTVSTISSRLREGGVYLITGG-----LGGLG 2213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2117 ---PEVGLLRGPVRVIPFEFPNLRLRLI-------DLDSADPIWRSGCEPLLRE 2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2062 PERDSPLARLEHLTELGFHHLLALARQLEAVGAPEVRLAVVTTGLAAIGGESELR----- 2116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 SMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPF------DMDSCLSR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 FHEPQVGLIQAAQQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLE----- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 PERGSRLCLYEDGTELTEDYFPSVPDNAE-----LVLLTLGQAWQGYVSDIRRFLSA 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09413814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGAEAQEEFLRVLG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89; Indels 67; Gaps
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CURRENT FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 20

LENGTH: 299

TYPE: PRT

ORGANISM: Drosophila melanogaster
US-09-069-023-20
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                                                                                                        QY
                                                                                                                                              Query Match
Best Local Similarity
Matches 22; Conserv
                                                                       12 KPFKVKDVTRNIKKAVCASSLEEIRSKVAEKFEKCDHLPTIHLDSDGTEIDDEEYFRTLD 71
72 ENTELVAVFPGEHW 85
                                 65 DNAELVLLTLGOAW 78
                                                                                                           6 KSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTEL-TEDYFPSVP 64
                                                                                                                                                   Conservative
                                                                                                                                              4.6%; Score 82.5; DB 4; Length 299; 29.7%; Pred. No. 1.6; ative 16; Mismatches 35; Indels
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Gaps

Search completed: May 26, 2003, 15:24:23 Job time: 23 secs

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Gencore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2003, 15:14:07; Search time 37 Seconds (without alignments) 878.201 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-748-451-2 1789 1 MLQKPKSVKLRALRSPRKFG.....SRIYKPQTRLKRKQPVRKRQ 338

ring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

26 27 28 29	2222222	76. 9 8 110 111 112 112 113 113 115 115 115 115 115 115 115 115	Result No.
88 89 55 55 55 55 55 55 55 55 55 55 55 55 55	91.5 91.5 91 91 91	98.5 98.5 98.5 98.5 93.5 91.5 91.5	Score 108.5 105.5 104 99.5
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A47563 T13719 T73636 T28896 A43554	E81573 E86527 A29329 C87555 B84497 T41702	A43803 A46027 I48128 VEHY S22119 I48771 AG3174 C38888 GNLJG5 S54784 A29176 D70441 A72046	ID A53188 T02213 JT0382 I46569 A25074
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glucose-6-phosphat calo protein - fru neuronal olfactome hypothetical prote desmin - African o	conserved hypothet CT234 hypothetical vimentin - chicken hypothetical prote hypothetical prote probable cation-tr	vimentin - mouse helicase IV (75 kD vimentin - Chinese vimentin - golden vimentin - rat slp(w7) - mouse (f acetolactate synth COI intron 10 prot HIV-1 retropepsin sex-limited protei sex-limited protei oxido/reductase ir	Description pericentrin - m NBS-LRR type re apolipoprotein apolipoprotein apolipoprotein

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85.5	86	86	86	. 86	86	86	86.5	87	87	87.5	87.5	88.5	88.5	88.5
		4.8	4.8	4.8	4.8	4.8	4.8	4.9	4.9	4.9	4.9	4.9	4.9	4.9
1744	2895	1571	1027	463	458	437	1121	1066	1066	1242	1035	1738	1306	1032
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C4HU	H85362	T14155	S37711	B43549	A43549	C75632	138127	T41099	T45283	S78061	GNLJGG	A24558	T13592	S12153
complement C4A pre	hypothetical prote	zinc finger protei	kinesin heavy chai	vimentin 4 - Afric	vimentin 1 - Afric	•	phosphoprotein pho	staurosporine targ	growth polarity ma	DNA-directed RNA p	HIV-1 retropepsin	complement C4 prec	hypothetical prote	pol polyprotein -

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ALIGNMENTS

RESULT 2 T02213 NBS-LRR type resistance protein - rice (fragment) C;Species: Oryza sativa (rice) C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 17-Nov-2000 C;Accession: T02213 R;Lesster, D; Kurth, J;; Laurie, D.A.; Yano, M; Sasaki, T.; Devos, K.; Graner, l/Proc. Natl. Acad. Sci. U.S.A. 95, 370-375, 1998 A;Title: Rapid reorganization of resistance gene homologues in cereal genomes. A;Reference number: Z14623; MUID:98081880; PMID:9419382 A;Accession: T02213 A;Accession: T02213 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-571 <lei></lei>	QY 108 CDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSG 154 Db 257 LSEQKVELEKIFQAKHEAEVSLKNLEAQHQAAIKKLQEDLQSEHCQYLQDLEQKFREKEK 316 Qy	Matches 56; Conservative 45; Mismatches 90; Indels 43; Gaps 11; Qy 2 LOKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYED 51	in - mouse Mus musculus (house mouse) 6.Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999. 6.Jan-1995 #text_change 05-Nov-1995 #text_change 05-Nov-1999. 6.Jan-1995 #text_change 05-Nov-1995 #text_change 05-Nov-1999. 6.Jan-1995 #text_change 05-Nov-1995 #text_change 05-Nov-1999. 6.Jan-1995 #text_ch
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A;Cross-references: E
C;Genetics:
A;Gene: r1
C;Superfamily: diseas
                                                           A;Gene: apoB
A;Introns: 39/3; 88/3; 159/2; 238/3; 1133/1; 1171/2; 1232/3
A;Note: the list of introns may be incomplete
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; cholesterol metabolism; LDL; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      apolipoprotein B - pig (fragments)
c;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Aug-1999
C;Accession: JT0382; I46567; I46568
R;Maeda, N; Ebert, D.L.; Doers, T.M.; Newman, M.; Hasler-Rapacz, J.; Attie,
                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Mesidues: 1-1778 <br/>
A; Residues: 1-1778 <br/>
A; Residues: 1-178 <br/>
A; Ebert, D.L.; Doers, T.M.; Newman, M.; Hasler-Rapacz, J.O.; Attle, Gene 69, 213-229, 1988
A; Title: Molecular genetics of the apolopoprotein B gene in pigs in relation to A; Reference number: 145567
A; Reference number: 145567
                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Molecular genetics of the apolipoprotein B gene A;Reference number: JT0382; MUID:89108006; PMID:2905687 A;Accession: JT0382
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A; Residues: 239-1778 <MA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 70,
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                                                                                                                                                                                                                   ecule type: DNA
sidues: 1-8,'5',10-238 <MA2
;Cross references: GB:M22646;
;Accession: 146568
                                                                                                                                               Cross-references: GB:M22647;
Comment: Apolipoprotein B is
   Query Match
Best Local Similarity
Matches 66; Conserv
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Best Local 9
                                                                                                                                     Genetics:
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                                                      ly: apolipoprotein B
atherosclerosis; cholesterol metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HDLAQSVSMDECLRLDDPP----NSSSTSRSSRHLSFSCHNRSRT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HNVSQNIAAE -- TRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FHKDYVFEKETLVQIWMALGFIQSPGRRTIEELGSSYFDELLGRSFFQHHKGGYVMHDAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPYSNRESRILESTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease resistance protein RPS2;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.L.; Doers, T.M.; Newman, M.; Hasler-Rapacz, J.; Attie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL:AF032688; NID:g2792219; PIDN:AAB96985.1; PID:g2792220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LFLMLRYLHVLELNRRDITELPDSI----GNLKMLRYLNLSGTGITVLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -TKDTEDDWKNVLRSEIWELPSDKNNILPALRLSYNHLPAILKRCFAFCSV
               5.8%;
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20.7%;
                                                                                                                                                                                                                                                   <MA2>
                                                                                                                                            NID:g164367; PIDN:AAA30997.1; PID: the predominant protein component
                                                                                                                                                                                                                                    NID: g164366; PIDN: AAA30996.1;
   52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
Score 104; DB:
Pred. No. 3.8;
52; Mismatches:
                                                                                                                                                                                                         from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 105.5;
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   123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                           Length 1778;
                                                         LDL; lipid binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
   Indels
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nent of the
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 98;
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 Gaps
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                                                                                                                                               low-density lips
                                                         lipoprotein
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C;Species: Sus
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C; Superfamily:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                  Conservative
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apolipoprotein B - pig (fragment)
C;Species: Sus scrofa domestica (domest
C;Date: 21-Feb-1997 *sequence_revision
                                                                                                                                                                                                                                                                                                                                                                      ATDFASQLSSQVEQFVQE----DIQEYLSILADADGKGKEKIAELSSRAQEII-KSWAV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSYLREVSSY-----PSTVG----AEAQEEFLRVLGSMCQRLRSMQYNGSYFDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEELTRLKEKKLADF IND IQQNINTTFNIYAPLGFRLLKENLDSPFGMLNEF IQNTLWEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFQLPGRARNYTGDELCNMVMTEVGEVLSQIYSKIHSGLEILLSYFQDLMEKSKLNKALK
                                                                                                                                                                                                                                                                                                                                                                                                                                    GAKGGSRLCTPEGWFSCQGPFDMDSCLS-----RHSINPYSNRESRILFSTWNLDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQELQQLHQYIKALRKEYFDPSMVGWTVKYYELEEKVINLIKNLVDVLK--DFHSKYTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKFTFDSVKYQLTDVVSEYGEQLKSLSQDVQKALSDLHSINITEILSELQIFLEGIFQEI 1523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFQLPER----GSRLC----
                                                                                                                                                                                                                                                                                                     IIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENL
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                                                                                                                                                                                                                                       TMKEIISNYHQR----FIYKLLDFSDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -VLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLC------
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apolipoprotein B - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 13-Aug-1999
C;Accession: I46569
R;Purtell, C.; Maeda, N.; Ebert, D.L.; Kaiser, M.; Lund-Katz, S.; Sturley, S.L.; Kodc
J. Lipid Res. 34, 1323-1335, 1993
A;Title: Nucleotide sequence encoding the carboxyl-terminal half of apolipoprotein B
A;Reference number: I46569; MUID:94014802; PMID:8409766
A;Recession: I46569
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2629 <PUR>
A;Cross-references: GB:L11235; NID:g164371; PIDN:AAA74655.1; PID:g951375
C;Genetics:
A;Gene: APOB

Superramily: apolipoprotein B

Query Match

5.6%; Score 99.5; DB 2; Length 2629;

Best Local Similarity 18.7%; Pred. No. 15;

Best Local Similarity 61; Mismatches 140; Indels 113; Gaps 16

Matches 72; Conservative 61; Mismatches 140; Indels 113; Gaps 16

RFQLPGRARNYTGDELCNMVMTEVGEVLSQIYSKIHSGLEILLSYFQDLMEKSKLNKARK ATDFASQLSSQVEQFVQE---DIQEYLSILADADGKGKEKIAQLSSRAQEII-KSWAV--GAKGGSRLCTPEGWFSCQGPFDMDSCLS-----RHSINPYSNRESRILFSTWNLDH SQELQQLHQYIKALRKEYFDPSMVGWTVKYYELEEKVINLIKNLVDVLK--DFHSKYTVS RSYLREVSSY------PSTVG-----AEAQEEFLRVLGSMCQRLRSMQYNGSYFDR EEELTRLKEKKLADFINDIQQNINTTFNIYAPLGFRLLKENLDSPFGMLNEFIQNTLWEA IKFTFDSVKYQLTDVVSEYGEQLKSLSQDVQKALSDLHSINITEILSELQIFLEGIFQEI 2374 ------VLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLC-----IIEKKRTIIPTLVEAI------KEQDGREVDWEYFYGLLFTSENLKLVHIVCHK----DEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRI---TMKEIISDYHQQFIYKLQDFSDQLSDYYE--KFIAETERLIDLSIQKYHM 260 2314 2594 2492 209 2434 108 2546 164 69

Query Match 5.5%; Score 99; DB 2; Length 466; Best Local Similarity 20.8%; Pred. No. 1.7; Matches 65; Conservative 47; Mismatches 111; Indels 90; Gaps 15; Matches 65; Conservative 47; Mismatches 111; Indels 90; Gaps 15; Oy 27 OEVLRKGCLREOLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86 180 EDIMRLREKLQEEMIQREEHNTLOSFRQDVDNASLARLDLERKVESLQEEI- 231 OY 87 RELSAFHEPOVGLIQAAQULLCDEQAPQRQRLLADLENVSNIAAETRAEDEPW 141 1	Title: Isolation of a human vimentin cDNA with a long 3'-noncoding region from a human ference number: I54056; MUID:90215314; PMID:2323579 cession: I54056 cession: I54056; MUID:90215314; PMID:2323579 A; Catus: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: I67-466 cRES> A; Cross-references: GB:M25246; NID:9240233; PIDN:AAA61282.1; PID:9340234 A; Cross-references: GB:M25246; NID:9240233; PIDN:AAA61282.1; PID:9340234 A; Genetics: A; Gene: GDB:VIM A; Cross-references: GDB:119630; OMIM:193060 A; Map position: 10p13-10p13 A; Introns: 188/2; 208/3; 240/3; 294/3; 336/3; 410/2; 425/1; 453/3 C; Superfamily: cytoskeletal keratin C; Keywords: colled coll; intermediate fllament; phosphoprotein	A; Residues: 113-200, 's',202-264,'S',266-277,'T',279-466 <per> A; Residues: 113-200, 's',202-264,'S',266-277,'T',279-466 <per> A; Note: the authors translated the codon GCG for residue 287 as Asp A; Note: the authors translated the codon GCG for residue, 287 as Asp R; Sommers, C. L.; Wallker-Jones, D.; Heckford, S.E.; Worland, P.; Valverius, E.; Clark, R. Cancer Res. 49, 4258-4263, 1989 A; Title: Vimentin rather than keratin expression in some hormone-independent breast cance and the common of the code of code and the code of co</per></per>	sidues: 1-466 <honv 'd',="" 'f',="" 1-41,="" 1986="" 3614-3620,="" 43-441,="" 443-466="" 6,="" <fer="" a25074="" a25074;="" a;="" and="" b.;="" battini,="" biol.="" calabretta,="" cell.="" coding="" de="" dna="" embl:x56134;="" ferrari,="" gene.="" growth="" human="" j.k.;="" kaczmarek,="" l.;="" mol.="" molecule="" muid:87089701;="" nid:g37849;="" number:="" of="" pid:g37850="" pidn:caa39600.1;="" pmid:3467175="" pross-references:="" r.;="" r;="" reference="" regulation="" residues:="" riel,="" rittling,="" s.;="" sequence="" the="" title:="" type:="" vimentin=""> A; Residues: 1-41, 'D', 43-441, 'F', 443-466 <fer> A; Cross-references: GB:M14144; NID:g340218; PIDN:AAA61279.1; PID:g340219 R; Perreau, J; Lilienbaum, A.; Vasseur, M.; Paulin, D. Gene 62, 7-16, 1988 A; Title: Nucleotide sequence of the human vimentin gene and regulation of its transcript A; Reference number: JT0234; MUID:88226018; PMID:3371665</fer></honv>	RESULT 5 A25074 C;Species; Homo sapiens (man) C;Date: 30 Jun-1988 #sequence_revision 10-May-1996 #text_change 13-Aug-1999 C;Accession: S13115; A25074; JT0234; S008487; I54056 R;Honore, B.; Madsen, P.; Basse, B.; Andersen, A.; Walbum, E.; Celis, J.E.; Leffers, H. Nucleic Acids Res. 18, 6692, 1990 A;Title: Nucleotide sequence of CDNA covering the complete coding part of the human vime A:Reference number: S13115; MUID:91067467; PMID:2251132 Ccession: S1318
A; Restricte number: 5.4-320 A; Accession: S14526 A; ACCESSION: S14526 A; ACCESSION: S155, 'EL', 158-163, 'F', 165-337, 'E', 339-466 < POD> A; Residues: 1-155, 'EL', 158-163, 'F', 165-337, 'E', 339-466 < POD> A; Cross references: EMBL: \$56397; NID: 955407; PIDN: CAA39807.1; PID: 955408 A; Cross references: EMBL: \$56397; NID: 955407; PIDN: CAA39807.1; PID: 955408 Biochemistry 28, 2974-2979, 1980 Biochemistry 28, 2974-2979, 1980 A; Title: Domain- and sequence-specific phosphorylation of vimentin induces disassembl A; Reference number: A31951; MUID: 89302884; PMID: 2500966 A; Accession: A31951 A; Molecule type: protein A; Residues: 5-12; 14-28; 37-69 < CAND> A; Accession: B31951	Molecule Residues: Cross-ref Hennekes J. Gen. G Title: Co Title: Co Title: Co Title: Co Totale: Co Title:		· · · · · · · · · · · · · · · · · · ·	Db 291 YKSKFADLSEAANRNNDALRQAKQESTEYRROVQSLTCEVDALKGTNESLEROMREMEEN 350 Oy 167 YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWESC 226 : : : :

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A; Molecule type: protein
A; Residues: 5-12;14-69 < AN2>
C; Superfamily: cytoskeletal keratin
C; Keywords: coiled coil; intermediate fi
F; 104-138/Region: coil 1A
F; 147-247/Region: coil 2A
F; 291-411/Region: coil 2A
F; 291-411/Region: coil 2A
F; 291-411/Region: coil 2A
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                                                                                                                                                                                                                                                                                                                                                                                                helicase IV (75 kD helicase) [imported] - Salmonella enterica subsp. enterica C;Species; Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 C;Accession: AF0627
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                                                                                                                                                                               A; Gene: STY1097
                                                                                                Query Match
Best Local S
Matches 89
                                                                                                                                                                                                                             ;Status: preliminary
;Molecule type: DNA
;Residues: 1-684 <PAR>
                                                                                                                                                              Superfamily: helicase
                                                                                                                                                                                                            Cross-references: GB:AL513382;
                                                                                                                                                                                                                                                                      re 413, 848-852, 2001
hors: Parry, C.; Quall, M.; Rutherford, K.;
le: Complete genome sequence of a multiple d
ference number: AB0502; PMID:11677608
Accession: AF0627
                                                                                                                                                                                                                                                                                                                                                                                       Parkhill,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,25,39,51,66/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase and p,10,21,26,34,42/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #statu7/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status expering
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                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFLKKLHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
    VLLTLGQAWQGYVSDI - - - RRFLSAFHEPQVGLI - - -
                                  CREIWRK-CLAWLQDSEGSRQQHNQAYADAMLEAHADFFTQIESSPLNPSQARAVVNGES
                                                                 CQEVLRKGCLRFQLPERGSRL---CLYEDG-TELTEDYFPSVPD------NAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEAIKEQDGREVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGPFDMDSCLSRHSINPYSNRESRI-----LFSTWNLDHI-----IEKKRTIIPTL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FALEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKSKFADLSEAANRNNDALRQAKQESNEYRRQVQSLTCEVDALKGTNVSLERQMREMEEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KMALDIEIATYRKLL---EGEESRISLPLPTFSSLNLRETNLESLPLVDTHSKRTL---L
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                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                     p.; Cronin, A.;
                                                                                                               22.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                              Score 98.5; DB
Pred. No. 3.1;
52; Mismatches
                                                                                                                                                                                                           PIDN:CAD08201.1; PID:g16502250; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                     K.D.; Thomson, N.R.;
Davis, P.; Davies, R.
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                                                                                                                               DB
                                                                                                                                                                                                                                                                                                      drug
                                                                                                148;
                                                                                                                                                                                                                                                                                                      Simmonds, M.;
drug resistant
                                                                                                                            2;
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                                                                                                                               Length
   -QAAQQLLCDEQAPQR---Q
                                                                                                Indels
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.M.; Dowd, L.;
                                                                                                                                                                                                                                                                                                     Skelton, J.; Stevens, K. Salmonella enterica serc
                                                                                                99;
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                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                     Wain, J.; Churcher; White, N.; Farrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
   116
                                  210
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A; Residues: 1-448 < RES>
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   hamster
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c;Species: Cricetulus griseus (Chinese C;Date: 04-Sep-1997 #sequence_revision C;Accession: I48L28 R;Bloemendal, H.; Quax, W.; Quax-Jeuken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M16718; NID:g191232; PIDN:AAA37029.1; PID:g387058
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                                              273 VEAIKEQDGREVD
                                                                                                                                                                                                                                                                                                                                                                                                     214 AFLKKLHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
                                                                                                                                                    QGPFDMDSCLSRHSINPYSNRESRIL----FSTWNLDHI----
IKTVETRDGQVIN
                                                                                                  KMALDIEIATYRKLL---
                                                                                                                                                                                                     FALEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ-----
                                                                                                                                                                                                                                                    YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC
                                                                                                                                                                                                                                                                                                     YKSKFADLSEAANRNNDALROAKQESNEYRROVOSLTCEVDALKGTNESLEROMREMEEN
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ilarity 20.1%;
Conservative (
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, 115-118, 1983
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                                                                                                ·EGEESRISLPLPNFSSLNLRETNLESLPLVDTHSKRTL---L
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Pred. No. 2;
47; Mismatches
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RESULT 10
$22119
vimentin - rat
vimentin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #seguence_revision 20-Feb-1995 #text_change 13-Aug-1999
C;Accession: $22119; JQ1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aperimental source: lans R;Chou, Y.H.; Ngai, K.L.; Goldman, R. J. Biol. Chem. 266, 7325-7328, 1991
J. Biol. Chem. 266, 7325-7328, 1991
A;Title: The regulation of intermediate filament reorganization in mitosis. p34(cdc2) ph A;Reference number: A39731; MUID:91210232; PMID:2019567
A;Accession: A39731
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C;Date: 19-Feb-1984 #sequence_revision 27-Rov-1985 #text_change 22-Jun-1999
C;Accession: A99842; A93953; A39731; A02959
C;Accession: A99842; A998353; A39731; A02959
R;Ouax, W.; Egberts, W.V.; Hendriks, W.; Quax-Jeuken, Y.; Bloemendal, H.
Cell 35, 215-223, 1983
A;Teitle: The structure of the vimentin gene.
A;Reference number: A90842; MUID:84026520; PMID:6194898
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A; Residues: 36-41'A', 42-47', 'T', 48; 49, 50-62; 63-67' <CHO>
A; Residues: 36-41'A' at the described as 40-Ser may be 41-Ser;
C; Comment: The initiator Met is not shown.
C; Comment: Vimentin occurs in intermediate-sized filaments in various
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C;Keywords: acetylated amino end; coiled coil; intermediate filament; phosphoprotein
F;411-464/Domain: tail <TLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 187/2; 207/3; 239/3; 293/3; 335/3; 409/2; 424/1; 452/3 C;Superfamily: cytoskeletal keratin
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Best Local (
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Comment: Vimentin occurs in intermediate-sized filaments in various nonepithelial cel
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Residues: 1-464 <QUI>
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                                                                                                                                                                                                                                                                                                    273 VEAIKEODGREVD 285
                                                                                                                                                                                                                                                                                                                                                               388 KMALDIEIATYRKLL---EGEESRISLPLPNFSSLNLRETNLESLPLVDTHSKRTL---L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 YKSKFADLSEAANRNNDALRQAKQESNEYRRQVQSLTCEVDALKGTNESLERQMREMEEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 EDIMR----LREKLQEE-----MLQREEAESTLQSFRQDVDNASLARLDLERKVESLQEEI- 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86
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Pred. No.
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                                                                                                Matches
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[148771]
Slp(W7) - mouse (fragment)
Slp(W7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I48771
                                                                                                                                                                                                                                                                                                                                       R;Hemenway, C.; Kalff, M.; Stavenhagen, J.; Walthall, D.; Robins, D.
Nucleic Acids Res. 14, 2539-2554, 1986
A;Title: Sequence comparison of alleles of the fourth component of complement (C4)
A;Reference number: I48274; MUID:86176748; PMID:3008092
A;Accession: I48771
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A;Experimental source: prostatic tumor; cell line Dunning R-3327; strain Fischer Cope C;Superfamily: cytoskeletal keratin C;Keywords: phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross references: EMBL:X62952; NID:g57479; PIDN:CAAA4722.1; PID:g57480
A;Experimental source: prostatic tumor; cell line Dunning R-3377; Strain Fischer Cope
R;Bussemakers, M.J.G.; Verhaegh, G.W.C.T.; Van Bokhoven, A.; Debruyne, F.M.J.; Schalk,
Blochem. Blophys. Res. Commun. 182, 1254-1259, 1992
A;Title: Differential expression of vimentin in rat prostatic tumors.
A;Reference number: JQ1389; MUID:92171936; PMID:1540169
A;Accession: JQ1389
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A;Description: differential expressions of vimentin in rat prostatic tumors: complete A;Reference number: S22119
A;Accession: S22119
                                                                                                                                                                                           A;MoLecule type; mRNA
A;Residues: 1-594 <RES>
A;Cross-references: EMBL:X06454; NID
C;Superfamily: alpha-2-macroglobulin
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                                                                                                                                        Query Match
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                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 VEAIKEODGREVD 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 QGPFDMDSCLSRHSINPYSNRESRIL-----FSTWNLDHI------IEKKRTIIPTL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 YKSKFADLSEAANRNNDALRQAKQESNEYRRQVQSLTCEVDALKGTNESLERQMREMEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 AFLKKLHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
18 KFGVAGRSCQEV-LRKG--CLRFQLPERGSRLCLY----EDGTELTEDYFPSVPDNAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86
                                                                                      l Similarity
58; Conserv
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                                                                                      Conservative
                                                                                                                                                                                                                         EMBL: X06454; NID: g54105; PIDN: CAA29760.1; PID: g54106
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24.1%; pre
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Pred. No.
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                                                                                      Mismatches
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CiAccession: AG3174
CiAccession: AG3174
CiAccession: AG3174
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Karp, P.; Romero, P.; Zhang, S.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58 A;Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 294, 2317-2323, 2
A; Authors: Yoo, H.; Tao,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
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Ate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
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         VRKRQ 338
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                                               ILGFQRDAETVKFGKYTTACHFAE-
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                                                                                 ----EQDGREVDWEYFYGLLFTSENLKLVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQP 333
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                                                                                                                                                                                                                                                                         -WRKFNDDR----RGY--YSSEASPLRPERIMAELQGVIDENTTVVAD
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Pred. No. 3.6;
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                                           VDHVKIAHACGCDAVRVTQPQDLKAHMQK 539
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                                                                                                                       WAELETLV---RMQIPITIIVLNNG
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C;Superfamily: pol polyprotein
C;Keywords: aspartic proteinase; hydrolase; nucleotidyltransferase;
F;106-204,Product: retropepsin *status predicted <RTP>
F;130/Active site: Asp (shared with dimeric partner) *status predict
                                                                                                   C; Genetics:
                                                                                                                   A;Cross-references: EMBL:M19499
C;Comment: Specific enzymatic c
                                                                                                                                                                                            R; Franchini, G.; Gurgo, C.;
Nature 328, 539-543, 1987
A;Title: Sequence of simian
A; Reference number: A28873;
A; Accession: B28873
                                                                                                                                                                                                                                                                                                                       HIV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus (African green N; Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed C; Species: simian immunodeficiency virus, SIV
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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Aug-2001
C;Accession: C38888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                               A; Gene:
                                                                                                                                                          A; Residues:
                                                                                                                                                                        A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: mitocl
F; 157-380/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Genetic code: SGC3
C;Superfamily: Podospora anserina mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-397 < CUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: C38888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: DNA sequence analysis of the 24.5 A; Reference number: A48327; MUID:90124722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Curr. Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Cummings, D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COI intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                           Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 03-Jun-200:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 QAAQQL----LCDEQAPQRORLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 protein - Podospora anserina mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 KILVIMDNPQITKARSENYKPGITEFLGLCM-----WVGISEAIRLLPTSLSKKIKDLI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 RLCLYEDGTELT----EDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLI 100
                                                                                                                                                          1-1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.J.; Michel, F.; McNally, K.L.
16, 381-406, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGDGCFQVSKKGYASLEIVTQLRDKRILYLIK-QKYGGAVKLHAGDNYLRYRLHHKAGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FALLQYSIRLEKGYFLMKNLKYSTLASDYSENSLANTRNKNNSPFKEKEDRFNEWLAGII 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPYSNRESRILFSTWNLDHIIEKKRTIIPTLVE-----AIKEQD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLINGINGLIRNPIRILQLGKICNLYDIKLKDTQPLTYYNGWLS--GFFDTDGSI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              --YLNEKSGQIFITAS----QKNRFILDALVELYGGTIYAMVKQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VLGSMCQRLRSMQYNG--SYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHSI 241
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                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                     Gurgo, C.; Guo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                          <FRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.2%;
                                                                                                                                                                                                                immunodeficiency virus and MUID:87287229; PMID:3497350
                                                                                                                   cleavages may yield mature proteins including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:M30937;
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                                                                                                                                                                                                                                                                       H.G.; Gallo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 93.5;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:M61734; NID:g14030;
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PMID:2558809
                                                                                                                                                                                                                                                                       R.C.;
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                                                                                                                                                                                                                                  its relationship to
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                                         polyprotein;
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	Overy Match 5.1%; Score 92; DB 2; Length 1735; Best Local Similarity 27.6%; Pred. No. 38; Matches 50; Conservative 20; Mismatches 63; Indels 48; Gaps 11; Qy 18 KFGYAGRSCQEV LRKG-CLKFQLDERGSRLCLYEDGTELTEDYFPSVPDNAEL 69	Molecule type: DNA Residues: 1-1735 <oga> Residues: 1-1735 <oga> Cross references: EMBL:M64933; NID:g. Cross references: EMBL:M64933; NID:g. Hemenway, C.; Kalff, M.; Stavenhagen notleic Acids Res. 14, 2539-2554, 1986 Title: Sequence comparison of allele: Reference number: I48274; MUID:86176 Accession: 148770</oga></oga>	ulus (house #sequence; #sequence; #148770 , N.E. 56-2763, 19 56-2763, 19 519 gene. S54784; M		119 -LADLLHNYSQNIAAETRAEDPPW-FEGLESRFQSKSGY	Query Match 5.2%; Score 92.5; DB 1; Length 1054; Best Local Similarity 22.8%; Pred. No. 18; Matches 56; Conservative 34; Mismatches 93; Indels 63; Gaps 11; Qy 13 LRSPRKFGVAGRSCQEVLRKGCLRFOLPERGSRLCLYEDGTELTEDYFPSVPDNAE 68
OY 18 KFGVAGRSCQEV-LRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAEL 69 : :	A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-21 <res> A;Cross references: GB:M14226; NID:g199615; PIDN:AAA39684.1; PID:g554239 A;Cross references: GB:M14226; NID:g199615; PIDN:AAA39684.1; PID:g554239 C;Genetics: A;Gene: Slp C;Superfamily: alpha-2-macroglobulin F;1-19/Domain: signal sequence #status predicted <sig> F;20-1736/Product: sex-limited protein #status predicted <mat> F;20-1736/Product: sex-limited protein #status predicted <mat> Ouery Match Best Local Similarity 27.6%; Pred. No. 38; Matches 50; Conservative 20; Mismatches 63; Indels 48; Gaps 11;</mat></mat></sig></res>			nce number: A94013; MUID:85038607; PMID:6208559 ion: B21692 ie type: mRNA es: 651-749, 'H',751-774, 'D',776-802,921-1040 <non> R.T.; Sepich, D.S. tl. Acad. Scd. U.S.A. 81, 4908-4911, 1984 Genes for murine fourth complement component (C4) and sex-lince number: A41195; MUID:84272739; PMID:6389636</non>	A;Title: Murine sex-ilmited protein; complete cDNA sequence and comparison with murin A;Reference number: A29176; MUID:86060918; PMID:3840826 A;Accession: A29176 A;Molecule type: mRNA A;Residues: 1-1756 <oga> R;Nonaka, M.; Takahashi, M.; Natsuume-Sakai, S.; Nonaka, M.; Tanaka, S.; Shimizu, A.; Proc. Natl. Acad. Sci. U.S.A. 81, 6822-6826, 1984 A;Title: Slocketion of cDNA clones specifying the fourth component of mouse complement</oga>	RESULT 16 A29176 Sex-limited protein precursor - mouse N;Alternate names: complement component C4-related sex-limited protein C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999 C;Accession: A29176; B21692; A41195; B29059; B60227; I79467 R;Ogata, R.T.; Sepich, D.S. J. Immunol. 135, 4239-4244. 1985

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C; Accession: A72096
R; Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, CNATURE Genet. 21, 385-389, 1999
A; Title: Comparative genomes of Clamydia pneumoniae and C. A; Reference number: A72000; MUID:99206606; PMID:10192388
                                                        A; Experimental source: strain C; Genetics: C; Genee: CP00293
C; Superfamily: Chlamydia traci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oxido/reductase
C;Species: Aquii
C;Date: 08-May-1
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D70441
                                                                                                                              A;Residues: 1-925 <ARN>
A;Cross references: GB:AE001614; GB:AE001363; NID:g4376562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xido/reductase iron sulfur protein - Aquifex aeolicus
;Species: Aquifex aeolicus
;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 17-Mar-2000
;Accession: D70441
                                                      Superfamily:
                                                                                                                                                  Residues: 1-925 <ARN>
                                                                                                                                                                                                                                                                                                    hypothetical protein - Chlamydophila pneumoniae (strain CWL029) ecies: Chlamydophila pneumoniae, Chlamydia pneumoniae pate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Ju-Accession: A72096
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: unassigned; 9-85/Domain: ferredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :Cross-references: GB:AE000748; NID:g2983960; PIDN:AAC07510.1; Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: DNA
Residues: 1-395 <AQF>
   Query Match
Best Local
                                                                                                                                                                                         Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           le: The complete genome of the hyperthermophilic bacterium erence number: A70300; MUID:98196666; PMID:9537320
 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 VDWEYF-YGLLFTSENLKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G.; Warren, P.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          K 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DWKVFSFTEIIANEDIEFKGKGEKVTVHVPCHYYTAMKLN--PNNFYKALGKVKNAETV 318
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                                                      trachomatis hypothetical protein
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 5.1%;
21.8%;
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                                                                                                               CWL029
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Pred. No. 5.9;
19; Mismatches
 Score
Pred.
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No. 1
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   18;
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                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
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                 Length 925;
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                                                        CT234
                                                                                                                                                                                                                                                                                J.; Olinger, L.;
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                                                                                                                                                                                                                                               trachomatis
                                                                                                                                PIDN: AAD18442.1;
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A;Title: Genome sequences of Chlamydia trachomatis MoPn and A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein CP0465 [imported] - Chlamyo C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-925 < REA>
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EQDGREVDWEY-FYGLL
                                                                      WFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPT-----LVEAIK
                                                                                                             KYAEAMIGELDKEVAPAFLQVL-
                                                                                                                                                                                                                        ----RAEDPPWFEGLESRFQ-----SKSGYLRYSCE-----SRIRSYLREVSSYPST--
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21.8%; Pred. No. 18;
                                     -LKKHAYKIVKSKASKALFYSYH-GHYIQKK----YPTYNLSLLANTLN
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; Kolonay, J.; McClarty, (
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A;Gene: CPj0293
C;Superfamily: Chlamydia trachomatis hypothetical protein CT234
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A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
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lecule type: DNA
sidues: 1-925 <STO>
sidues: 1-925 <STO>
foss-references: GB:BA000008; NID:g8978667; PIDN:BAA98503.1; GSPDB:GN00142
;Experimental source: strain J138
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782 SNYYAEVNFMLSLLGILGSMEHSGYLIRALTSKNOK---IKAQALESLEKNCD 831
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                                                                278 EQDGREVDWEY-FYGLL------FTSENLKLVHIVCHKKTTHKLNCD 317
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Search completed: May 26, 2003, 15:23:48 Job time: 40 secs

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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Match Length
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Q9U786
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Q9CZL3
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048991 oryza sativ
09cz13 mus musculu
029433 sus scrofa
09u786 drosophila
029021 sus scrofa
08zq65 salmonella
08zq77 salmonella
062238 mus musculu
060819 homo sapien
                                                                                                                         Q8uvs5 gallus gall
Q9dg17 brachydanio
Q96p72 homo sapien
Q96p74 homo sapien
Q96p73 homo sapien
Q96p73 homo sapien
Q9v3h0 drosophila
Q9ndr2 drosophila
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	Q9xyd1 drosophila	096958 drosophila			5	Ω	ω	0	Q96wt6 schizosacch	0						Q9vwb9 drosophila		090317 chimpanzee	Q9z8p5 chlamydia			067558 aquifex aeo	-			Q02689 podospora	0	-	Q8ukh9 agrobacter

ALIGNMENTS

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Qy Db	y 0y	Ma Do	SQ	닭	DR DR	RL	집	RA	₽;	R	R C	8	8	გ	O N	DE	ğ	ij	AC	ID Q	RESULT
6 KGFKLKKEGSAUNFUAAAGSJANGLIKNGURLIANDELANGSRUGJIEDOSEGERIKEE OO 66 NAELVILITIGQAWQGYVSDIRRFILSAFHEPQVGLIQAAQQLICDEQAPQRQRLIADLIHN 125		Query Match 58.3%; Score 1043; DB 13; Length 333; Best Local Similarity 60.1%; Pred. No. 7.8e-86; Matches 197; Conservative 51; Mismatches 74; Indels 6; Gaps 2;	SEQUENCE 333 AA; 38474 MW; 9B069CD287755E11 CRC64;	Pfam; PF02017; CIDE-N; 1.	EMBL; AF406/61; AAL3//16.1; . InterPro: IPR003508; CAD.	J. Biol. Chem. 276:45427-45432(2001).	"CAD/DFF40 Nuclease Is Dispensable for High Molecular Weight DNA Cleavage and Stage I Chromatin Condensation in Apoptosis.";	Samejima K., Tone S., Earnshaw W.C.;	PubMed=11577114;	SECUTENCE FROM N.A.	TIT TRANSPORT	Gallus.	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	<pre>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</pre>	CAD. Gallus gallus (Chicken).	ase-acti	01-JUN-2002 (Transfire). 21, Last annotation update)	(TrEMBLrel. 20,	•	Q8UVS5 PRELIMINARY; PRT; 333 AA.	LT 1

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Ol-MAR-2001 (TrEMBLrel. 16, Last son ol-MAR-2001 (TrEMBLrel. 16, Last son ol-MAR-2001 (TrEMBLrel. 16, Last annotation upon ol-MAR-2002 (TrEMBLrel. 20, Last annotation upon ol-MAR-2002 
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Matches 169
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Submitted (SEP-2001) to the EMBL/GenBank/
EMBL; AF286179; AAE99706.1; -
EMBL; AF426316; AAL40264.1; -
HSSP; 000273; ILBX.
InterPro; IPR003508; CAD.
Pfam; PF02017; CIDE-N; 1.
SMART; SM00266; CAD; 1.
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HIVCHKKTTHKLNCDPSRIYKPQTRLKR
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                                                                                                                                    PYSNRESRILFSTWNLDHIIEKKRTIIPTLYEAIKEQDGREYDWEYFYGLLFTSENLKLY 302
                                                                                                                                                                                                                                KSEYKKVAEALAEKLKAARYNGTYFDRSEKDANRLCTEEGWFSCQGAFDENSCNFLHSIN
                                                                                                                                                                                                                                                              SNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYEYGLLFTSENLKLVHI 304
                                                                                                  PYGNRESRILFSTWNLDHLIEKKRTVIPALAKALEANKSNDINVDYFYKLLFTRENLKLV
                                                                                                                                                                                                                                                                                                                                                             SNLRDRSELENRLODHDWFEGIDTRFKTKSAYMKYNCESRIRGYLKEVDGYTQTIKNAKT
                                                                                                                                                                                                                                                                                                                                                                                                                              HNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTV-GAEA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDNTDLVLLPHGQSWNGFADEINRVLGLDRNTEELLVSAAQGLLSDERSPKRRRILGDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLADLL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPKLVKIRSANQARKYGIAAVNLKELIKKGCQLLKVSSSGVLVCLYEDGTVVTEEYFQNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YKRILDLMSDKLKSVKYNGSYFDRTEEEAAMRLCTKEGWFSCQGPFDRDDCPCKHSINPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 941;
Pred. No. 1
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1.2e-76;
nes 88;
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Q96P72;
01-DEC-2001
01-DEC-2001
01-MAR-2002
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01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                          Bayascas J.R., Yuste V.J., Perera R., Comella "Characterization of splice variants of human that show CIDE-N structure and function."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AF409060; AALO2005.1; -. InterPro; IPR003508; CAD. Pfam; pF02017; CIDE-N; 1. SEQUENCE 110 AA; 12106 MW; 34E72888A0F3B90
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Bayascas J.R., Yus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                  08;
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   PSVPDNAELVLLTLGQAWQG
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                                                          MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF
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1 (TrEMBLrel. 19,
2 (TrEMBLrel. 20,
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(TrEMBLrel. 19, Last sequence of the control of the cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Human).
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Primates;
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Primates;
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Last annotation update)
truncated form III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
truncated form I.
                                                                                                                                                                         Score 419; DB 4; 1
Pred. No. 3.3e-30;
0; Mismatches 0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                    34E72888A0F3B909 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                     databases
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caspase-activated
                                                                                                                                                                                                                                      Length 110;
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PSVPDNAELVLLTLGQAWQG

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RESULT 5
Q96P73
ID Q96P
AC Q96P
DT 01-D
DT 01-D
DT 01-M
DT 01-
          RAPAX CRAPARA RELATION OF COMMENTAL REPORT OF 
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Best Local S
Matches 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REP4 protein (CG9414 protein).
REP4 OR DCAD OR CG9414.
Drossophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09V3H0;

01-MAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEDLINE-20166006: PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bayascas J.R., Yuste V.J., Perera R., Comella J.X.; "Characterization of splice variants of human caspase-activated DNase that show CIDE-N structure and function."; Submitted (AUG-2001) to the EMBI/GenBank/DDBJ databases.

SUBBL; AF409061; BAL02006.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
DNA fragmentation factor B truncated form II.
                                                                                                                                                                                                                                                                                                                                                                       Inohara N., Nunez G.;
Submitted (NOV-1999)
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20085845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nonhara N., Nunez G.;
'Genes with homology to DFF/CIDEs found in Drosophila melanogaster.";
Jell Death Differ. 6:823-824(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=10627165;
G.;
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; Pred. No. 3.5e-30;
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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Apbayani A., An H.-J., Andrews Pfennkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M.,
RA HITLIS K.C., Busam D.A., Butler H., Cadieu E., Devis P.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davis P.,
RA Colson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA RA College C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Cham R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Welman P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Welminson J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Melnot N., Melson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nursy M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Melson D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA M
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Best Local
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                                                                                                                           281 RIPSKRLRQVIREYTKENCILDEWSTSLCSDLGDFYCQGSYSENGNSCSKQHTINPYASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106;
                                                                                                                                                                                                                                                                                                                                                                                                                           76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 RKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTED-YFPSVPDNAELVLLTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                               NSKTHLSLKAEHVEWFTGGEERFHSKEEAMATRAQTRVRGYY-----YKAKEEL
                                                                                                                                                                                                                                                                                                                                         ET-----RAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGAEAQEEF 186
                                                                                                                                                                                                                                                                                                                                                                                                            QAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCD--EQAPQR-QRLLADLLHNVSQNIAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKYGIGANSLEMLIAKAKSKFPLLE--PHLYLASDGFEVSDDEYLKSLP--AQTLFIVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00190; (
                                       ENLILFQVWNLDHQIELCRTILPALVANVEELVSHPQTKCSIHKKQVVDISVLEYFLE-I
                                                                                 ESRILFSTWNLDHIIEKKRTIIPTLVEAIKE------QDGREVD---WEYFYGLL
FTSENLKLVHIVCHKK-----TTHKLNCDPSRIYK 323
                                                                                                                                                                                                             TRNPLYRQNAKARQVINSVLEKFRYLLIGCDFFSMMFDRNCKQKHEFLKQHLGDEETDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                       -----VLGSMCQRLRSM----QYNGSYFDRGAK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOCHROME_C; UNKNOWN_1.; 52017 MW; CBAA690902178BAB CRC64;
                                                                                                                                                                 17.9%;
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Pred. No. 1.
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RESULT
048981
ID 04
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Best Local
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048981;
01-JUN-1998
01-JUN-1998
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SEQUENCE FROM N.A.
MEDLING-20239953; PubMed-10777599;
MEDLING-20239953; PubMed-10777599;
"^bovama H., Mukae N., Sakahira H., Okawa K., Iwamatsu A.
"^bovama H., mukae N., Sakahira H., Okawa K., Iwamatsu A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9NDR2;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.",
J. Biol. Chem. 275:12978-12986(2000).
EMBL; AB036773; BAA$7120.1; -.
FlyBase; FBgn0028406; Rep4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caspase-activated DNase. REP4 OR DCAD OR CG9414.
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InterPro; IPR000345; CytC_heme_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
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; SM00266; CAD; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106;
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                                                                                                FSLKNLKLVHIVCHEKAQRSNRSNGRLLCSDCHEYR 435
                                                                                                                                                                                                          RIPSKRLRQVIREYTKENCILDEWSTSLCSDLGDFYCQGSYSENGNSCSKQHTINPYASR
                                                                                                                                                                                                                                                            TRNPLYRQNAKARQVINSVLEKFRYLLIGCDFFSMMFDRNCKQKHEFLKQHLGDEETDAG
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                                                                                                                                                       ENLILEQVWNLDHQIELCRTILPALVANVEELVSHPQTKCSIHKKQVVDISVLEYFLE-I
                                                                                                                                                                               ESRILFSTWNLDHIIEKKRTIIPTLVEAIKE------QDGREVD---WEYFYGLL
                                                                                                                                                                                                                                                                                                               NSKTHLSLKAEHVEWFTGGEERFHSKEEAMATRAQTRVRGYY---
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  (TrEMBLrel.
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                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                      -VLGSMCQRLRSM----QYNGSYFDRGAK-----
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 Created)
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Pred. No. 1.8e-20;
1; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3D3E4E10AB32E48D
                                                                                                                                                                                                                                 -GGSRLCTPEGWFSCQGPF--DMDSCLSRHSINPYSNR
 sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
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Best Local S
Matches 69
                                                                                    Q9CZL3;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11 days embryo cDNA, RIKEN full-length enriched lib.
clone:2700062L12, full insert sequence.
                                                                            VIM.
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EMBL; AF03268; AAB96985.1; -.
InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).

Gukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.

MCBI_TaxID-4530;
SEQUENCE FROM N.A
                        NCBI_TaxID-10090;
                                     Eukaryota;
Mammalia; ]
                                                Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                   Q9CZL3
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Leister D., Kurth J., Laurie D.A.,
Graner A., Schulze-Lefert P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NBS-LRR type resistance protein (Fragment). R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00560; LRR; 3.
Pfam; PF00931; NB-ARC; 1.
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                                                                                                                                                                                                                                                                                                                                                              AQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHSI 241
                                                                                                                                                                                                                                                                                                                                                                                                                HNVSQNIAAE--TRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSLLC----TKDTEDDWKNVLRSEIWELPSDKNNILPALRLSYNHLPAILKRCFAFCSV
                                                                                                                                                                                                                                   SIGRLFNLQTLKL----
                                                                                                                                                                                                                                                            -YGLLFTSENLKLVHIVCHKKTTHKLNCDPSRI
                                                                                                                                                                                                                                                                                                            NPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FHEPQV---
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                                     Eutheria;
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571 AA;
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                                                                                                                                                                   PRELIMINARY;
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                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                      LFLMLRYLHVLELNRRDITELPDSI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64503 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.9%; Score 105.5; 20.7%; Pred. No. 0.
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                                                                                                                                                                                                                                   KNCHVLECIPGSI
                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                   PRT;
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a; Poales; Poaceae;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Wishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kuchi T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
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RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Gustincich S., Kinepala M., Kaniya K.H., Weitz C., Whitaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                            Q29433
Q29433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21085660;
                                                                                         01-NOV-1996 (TremBLrel. 01, 01-NOV-1996 (TremBLrel. 01, 01-NOV-1998 (TremBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01248; TYPELKERATIN. PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001664; IF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AK012469; BAB28263.1; -. MGD; MGI:98932; Vim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
  Eukaryota;
                                                                   Apolipoprotein B (Fragment)
                        scrofa
                                                                                                                                                                                                                                                                                                      273 IN 274
                                                                                                                                                                                                                                                                                                                                              284 VD 285
                                                                                                                                                                                                                                                                                                                                                                                               219 RKLL---EGEESRISLPLPTFSSLNLRETNLESLPLVDTHSKRTL---LIKTVETRDGQV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 VGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 ANRNNDALRQAKQESNEYRRQVQSLTCEVDALKGTNESLERQMREMEENFALEAANYQDT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 ----EGLESRFQSKSGYLRY------SCESRIR----SYLREVSSYPST 177
                                                                                                                                                                                                                                                                                                                                                                                                                                          238 RHSINPYSNRESRI-----LFSTWNLDHI------IEKKRTIIPTLVEAIKEQDGRE 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 QELQAQIQEQHVQIDVDVSKPDLTAALRDVRHEY-ESVAAKNLQEAEEWYKSKFADLSEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 QLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 GLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWF------ 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RIREKIQEEMIQREEAESTIQSFRQDVDNASIARLDLERKVESIQEEI-AFIKKIHDEEI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coil;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 AA;
(Pig).
Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Intermediate filament
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%; Score 104.5;
20.2%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                      Created)
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                                                                                                                                                                                       1540 AA
     Vertebrata;
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                                                                                           update)
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     Euteleostomi;
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RESULT 11
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MEDLINE-89108006; PubMed-2905687;
MEDLINE-89108006; PubMed-2905687;
Maeda N., Ebert D.L., Doers T.M., Newman M., Hasler-Rapacz J.,
Attle A.D., Rapacz J., Smithies O.;
"Molecular genetics of the apolipoprotein B gene in pigs in relation
to atherosclerosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
NCBI_TaxID-9823;
                                                                                                                                                                                                        Q9U786; PRELIMINARY;
Q9U786;
01-MAY-2000 (TIEMBLITEL 13,
01-MAY-2000 (TIEMBLITEL 13,
01-JUN-2001 (TIEMBLITEL 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maeda N., Ebert D.L., Doers T.M., Newman M., Hasler-Rapacz J.,
Attie A.D., Rapacz J., Smithies O.;
"Molecular genetics of the apolipoprotein B gene in pigs in relation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 70:213-229(1988).
                                                                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                         Ephydroidea; Dro
NCBI_TaxID-7227;
                                                                                                                                                                            REP3 OR DREP3 OR CG8364.
                                                                                                                                                                                          DREP3
                                                MEDLINE-20085845;
                                                               SEQUENCE FROM N.A.
 Inohara N., Nunez G.;
"Genes with homology to DFF/CIDEs :
Dell Death Differ. 6:823-824(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1286
                                                                                                                                                                                                                                                                                                                                                                                                                     1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1166 RFQLPGRARNYTGDELCNMVMTEVGEVLSQIYSKIHSGLEILLSYFQDLMEKSKLNKALK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                    IIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENL 299
                                                                                                                                                                                                                                                                                                                                                                                                                   ATDFASQLSSQVEQFVQE---DIQEYLSILADADGKGKEKIAELSSRAQEII-KSWAV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAKGGSRLCTPEGWFSCQGPFDMDSCLS-----RHSINPYSNRESRILFSTWNLDH 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQELQQLHQYIKALRKEYFDPSMVGWTVKYYELEEKVINLIKNLVDVLK--DFHSKYTVS 1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSYLREVSSY-----PSTVG----AEAQEEFLRVLGSMCQRLRSMQYNGSYFDR 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEELTRLKEKKLADFINDIQQNINTTFNIYAPLGFRLLKENLDSPFGMLNEFIQNTLWEA 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DEQAPORORLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRI--- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------VLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLC-----
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1540 AA; 174656 MW; 1E67510A18582F0E CRC64;
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                                                                                                            Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=2905687;
                                              PubMed=10627165;
                                                                                                                                                                                                                                                                                                                                                        -TMKEIISNYHQR-----FIYKLLDFSDQL 1481
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                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                           PRT;
                found in
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                Drosophila melanogaster.";
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                                                                                                                               Brachycera;
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                                                                                                                               Muscomorpha;
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Best Local
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                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                "Nucleotide sequence encoding the carboxyl-terminal half apolipoprotein B from spontaneously hypercholesterolemic J. Lipid Res. 34:1323-1335(1993).

EMBL; L11235; AAA74655.1; -.
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01-NOV-1996 (TremBLrel.
01-мак-2002 (TremBLrel.
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InterPro; IPR003508; CAD.
Pfam; PF02017; CIDE-N; 1.
SMART; SM00266; CAD; 1.
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                                                                                                                                                                                                                  ry Match
                                                                                                                                                                                                                                                    Lipoprotein.
NON_TER
                                                                                                                                                                                                                                                                          InterPro; IPR000510; Oxred_nitrognse1
Pfam; PF00148; oxidored_nitro; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q29021;
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                                                                                                                                                                                                                                                                                                                                                            Purtell C., Maeda N.,
Sturley S.L., Kodoyian
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=94014802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa
                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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  2435
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Q9UHD4; 1D4B.
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                                                                                                                                                                                                     Similarity
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SQELQQLHQYIKALRKEYFDPSMVGWTVKYYELEEKVINLIKNLVDVLK--DFHSKYTVS
                      RSYLREVSSY-------PSTVG----AEAQEEFLRVLGSMCQRLRSMQYNGSYFDR
                                                                                              IKFTFDSVKYQLTDVVSEYGEQLKSLSQDVQKALSDLHSINITEILSELQIFLEGIFQEI
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                                                                    -DEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRI---
                                                                                                                                          REQLPGRARNYTGDELCNMVMTEVGEVLSQIYSKIHSGLEILLSYFQDLMEKSKLNKARK
                                                                                                                                                                   RFQLPER----GSRLC---
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                                                                                                                    -------VLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDNSKPFKIKDITRNIRKAVVATTLSELRTKVSLKFERAQR--RLHLDCDGTEVDDEEYF
                                                                                                                                                                                                                                       2629 AA;
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                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  PubMed=8409766;
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25.5%;
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                                                                                                                                                                                                     5.6%;
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01,
20,
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                                                                                                                                                                                                     Score 99.5;
Pred. No. 1
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Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                            Grunwald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5A9975BCA8AFA645 CRC64;
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                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                       5389C4CC17A87049 CRC64;
                                                                                                                                                                                                                                                                                                                                                         Kaiser M., Lund-Katz wald K., Nevin D.N., &
                                                                                                                                                                 -----LY---EDGTELTEDYFPSVPDNAEL-----
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RESULT 13
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Best Local S
Matches 89
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                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE008746; AAI20008.1; -.
InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
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Courtney L., Porwollik S., Ali J., Dante M., Du F., Ho
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-LT2 / SGSC1412 / ATCC 70072
MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella typhimurium
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete genome sequence of Salmonella
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EFQDISPQRAALLEALRKQNSQTTLFAVGDDWQAIY--RFSGAQLSLTTAFHQTFGEGEH
                                                   ECRELFGKRIKLMAPLLKAWKSALKAENAVDFS--GLIHQAMVILEKGRFISPWKHILVD
                                                                             SCQGPFDMDSCLSRHSINPYSN---RESRILFSTWNLDH----IIEKKRTIIP-----
                                                                                                          WLEEEMQWVVPEGNFWDDETLQRRLAPRLDRWVSLMRMHG-----GAQAEMIAGAPE---
                                                                                                                                                            EITARTFHSLALYI-IQQGSKKAPVVSKLESDATARHQLFLRTWRQQCSEKKAQAKGWRQ 327
                                                                                                                                                                                         RLLADLLHNVSQNIAAETRAEDPPWFEGLES----RFQSKSGYLRYSCESR-----IRS
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                        -TLVEAIKEQDGREV-----DWEYFYGLLFTSENLKLVHIV--
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20, Last sequence update)
21, Last annotation updat
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Pred. No. 3
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RESULT 14
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AC Q8Z7R
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Baker S., Baylam D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamin N., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
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01-MAR-2002 (TrEMBLrel. 20; Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Helicase IV (75 kDa helicase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicase; Complete proteome. SEQUENCE 684 AA; 78038 MW; 5E9077CD302A198E CRC64;
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"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Pfam; PF00580; UvrD-helicase; 1.
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                                                                                                    496 CHLDTTYRFN---SRIGDIANRFVQQNP 520
                                                                                                                                                                        306 CHKKTTHKLNCDPSRIYKPQTRLKRKQP 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 CREIWRK-CLAWLQDSEGSROOHNQAYADAMLEAHADFFTQIESSPLNPSQARAVVNGES 210
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060819
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Best Local S
Matches 58
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062238; Ol-NOY-1996 (TrEMBLrel. 01, Created)
01-NOY-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Sex-limited protein Slp(w7) alpha-gamma chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      060819
                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                             (Fragment).
                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 20, Last annotation update)
DJ934G17.1.2 (Chloride chanel protein CLC-6B) (Isoform
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases EMBL; AL021155; CAA15952.1; -.
                                Errington H. Submitted (M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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InterPro; IPR001134; Netrin_C.
Pfam; PF00207; A2M; 1.
Pfam; PF01759; NTR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 14:2539-2554(1986).
EMBL; X06454; CAA29760.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hemenway C., Kalff M., Stavenhagen J., "Sequence comparison of alleles of the "Get and sex-limited protein (SL).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=B10.D2(C4(H)SLP(A));
MEDLINE=86176748; PubMed=3008092;
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                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386 V-----GF------GASQEVVVGLVQPSSAVLYDYYSPDHKCSVFYAAPTKSQL 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 KLGLSGMAIADITLLSGFHALRGDLEKLTSLSDRYVSHFETDGPHVLL-YFDSVPTTREC 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    486 GRAAFRLFESKITQVLHFRTDTMASIG-----QTRNFLSRTSCRLR-LEPNKEYLIMGMD 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 -----ESRIRSYLREVSSYPSTYGAEAQEEFLRYLGSMCQRLRSMQYNGSYFDRGAK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        429 LATL---CSGDVCQCAQGKCPPLLRSLERRVEDKDGYRMRFACYYPRVEYGFTVKVLRED 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 LADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGY-LRYSC------ 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 VLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCD------EQAPQRQRL 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 F
594 F
66454 MW;
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                                                                                                                                                                                                    Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271
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fourth component of complement
                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 594;
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                                                                                                                                                                                                         Hominidae;
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RESULT ORIUKING PROBURTS OF THE PROBUS PROBU
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SECUENCE F. MOOD G.E., Almeida N.F. Jr., Woo L.

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyarin T., Levy R., Li M.-J., McClelland E., Palmleri A.,

Kutyarin T., Levy R., Li M.-J., McClelland E., Palmleri A.,

Kutyarin T., Levy R., Li M.-J., McClelland E., Palmleri A.,

Kutyarin T., Levy R., Li M.-J., McClelland E., Palmleri A.,

Kutyarin T., Levy R., Li M.-J., McClelland E., Fomero P., Gordor

Kutyarin T., Levy R., Li M.-J., McClelland E., Fomero P., Gordor

Kutyarin T., Levy R., Li M.-J., McClelland E., Fomero P., Gordor

Kutyarin T., Levy R., Li M.-J., McClelland E., Follow R., Perry J.

Kutyarin T., Levy R., Li M.-J., McClelland E., Follow R., Perry J.

Kutyarin T., Levy R., Li M.-J., McClelland E., Follow R., Perry J.

Kutyarin T., Levy R., Li M.-J., McClelland E., Follow R., Perry J.

Kutyarin T., Levy R., Li M.-J., McClelland E., Follow R., Perry J.

Kutyarin T., Levy R., Li M.-J., McClelland E., Follow R., Perry J.

Kutyarin T., Levy R., Li M.-J., McClelland E., Follow R., Perry J.

Kutyarin T., Levy R., Li M.-J., McClelland E., Follow R., Perry J.

Kutyarin T., Levy R., Li M.-J., McClelland E., Follow R., Follow R.
"Genome sequence of the plant pathogen Agrobacterium tumefaciens C58."; Science 294:2323-2328/2001
                                                                                                                      Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., M. Houmiel K., Gordon J., Yaudin M., Iartchouk O., Epp A., Liu Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Mar Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gordon-Kamm B., Liao L., Chumley F., Tingey S.V., Nester E.W.;
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ATRC OR ATU5123 OR AG
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01-JUN-2002 (TrEMBLrel.
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Pfam; PF00654; voltage_CLC; 1.
                                                                                                                                                                                                                                                                                                                                                                                          Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 1.3;
35; Mismatches
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01-NOV-1998
01-MAR-2002
                                                                     NON_TER
                                                                                       Pfam; PF00207; A2M; Pfam; PF01759; NTR;
                                                                                                         Submitted (JUN-1998) to the EMBL/Ge
EMBL; AB015623; BAA31154.1; -
InterPro; IPR001599; Macroglobina2
InterPro; IPR001134; Netrin_C.
                                                                                                                                                                  STRAIN-F1 ANIMALS OF C57BL6
Matsumoto K., Ikuta T.;
"Mus musculus 5' truncated
                                                                                                                                                                                                                                                                                                         088305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE008936; AAL45813.1;
EMBL; AE007884; AAK90497.1;
Plasmid; Complete proteome.
SEQUENCE 571 AA; 62030 M
                                                                                                                                                 hydroxylase (Cyp21), and and complete sequences.";
                                                                                                                                                                                                                             Eukaryota;
Mammalia; 1
                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                                                                                                                    088305
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                                                                                                                                                                                                EQUENCE FROM N.A.
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KFGVAGRSCQEV-LRKG--CLRFQLPERGSRLCLY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKKRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DGGFA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASYSSMWVLGQLRISSERTRVLT-----PRGLAGLGWGVPLAIGAKVAAPESDVVALVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REAVCHRLRES--WRKFNDDR----RGY--YSSEASPLRPERIMAELQGVIDENTTVVAD
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                                                                                                                                                                                                                            ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQEEFLRVLGSM---CQRLRSMQYNGSYFDRGAKG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTW-NLDHIIEKKRTIIPTLVEAIK--
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                               Conservative
                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                               (Mouse)
                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                  544
                                                                                                                                                                                                                           Chordata;
Rodentia;
                                                                     43649 MW;
                                                                                                                                                                                                                                                                   (Fragment).
                                      5.3%;
                                                                                                                                       to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                      C57BL6
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Last
                             Score 95; DB
Pred. No. 2.9;
21; Mismatches
                                                                                                                                                                                      AND CBA CROSS;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                   PRT;
                                                                     EE2AA97B15597047 CRC64;
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No. 3.
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2.9;
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                                                 Length
  -EDGTELTEDYFPSVPDNAEL
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; Murinae; Mus
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                              48;
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RESULT 20
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Q02689;
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Q1-NOV-1996
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes Cells 6:237-247(2001).
EMBL; AB003040; BAB85589.1; -.
SEQUENCE 1572 AA; 178396 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21160571; PubMed-11260267;
Kohda T., Asai A., Kuroiwa Y., Kobayashi S., Aisaka K., Nagashima G.
Yoshida M.C., Kondo Y., Kaglyama N., Kirino T., Kaneko-Ishino T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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les 63; Conserv
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                                                                                                                                                                                                                                                                                                              326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 TSRGLKPMPEAKKPSHRRGICEDESSHGVIMEKFIKDVARNPKSGRARELNERPPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 YQNVVELKEDKKPQNPIQDNLENYRKLLSLGVQLAEDDRHSHMTQGHSSRSKR--TAYPS 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 YEDGTELTEDYFPSVP--DNAE--LVLLTLG------QAWQGYVSDIRRFLSAFHE 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---RFPRPNDNWKDSSSSRRESVIQE-RGYEGS----AFRGGFRFNADLASRSRALERKR 268
                                                                                                                                                                                                                                                                                                           VCDECGRQFSVISEFVEHQ------IMHTRENLYEYGESFIHSV 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SY-FD---RGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDH 260
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InterPro; IPRO01982; Endonuc_LAG/HNH.
Pfam; PF00961; LACIDADG_L; 2.
Hypothetical protein; Mitochondrion.
SEQUENCE 397 AA; 45576 MW; 6D736E89C2D15A7C CRC64;
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Sordariales; Lasiosphaeriaceae; Podospora.
NCBI_TaxID=5145;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cummings D.J., McNally K.L., Domenico J.M., Matsuura E.T.;
"The complete DNA sequence of the mitochondrial genome of Podospora
anserina ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical 45.6 kDa protein in COI intron 10 region Podospora anserina.
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                                                                                                                189 -----VLGSMCQRLRSMQYNG--SYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHSI 241
                                                                                                                                                         163 DGDGCFQVSKKGYASLEIVTQLRDKRILYLIK-QKYGGAVKLHAGDNYLRYRLHHKAGLL 221
275 --YLNEKSGQIFITAS-----QKNRFTLDALVELYGGTIYAMVKQD 313
                                         242 NPYSNRESRILFSTWNLDHIIEKKRTIIPTLVE-----AIKEQD 280
                                                                             222 SLINGINGLIRNPIRILQLGKICNLYDIKLKDTQPLTYYNGWLS--GFFDTDGSI-----
                                                                                                                                                                                                151 -----SKSGYLRYSCESRIRS----YLREVSSYPSTVGAEAQEEFLR-----
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                                                                                                                                                                                                                                                                            101 QAAQQL----LCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQ------
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                                                                                                                                                                                                                                                                                                                   49 KILVIMDNPQITKARSENYKPGITEFLGLCM------WVGISEAIRLLPTSLSKKIKDLI 102
                                                                                                                                                                                                                                                                                                                                                       45 RLCLYEDGTELT----EDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLI 100
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Search completed: May 26, Job time: 68 secs 2003, 15:22:58

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SUMMARIES

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Listing first 45 summaries
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1: 9319279Cgddta/geneseq/geneseqn-embl_NA1980.DAT:*

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Ygapop 10.0 , Ygapext
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                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a human DNA fragmentation factor subunit of 40 kDa, designated DFF40. The specification also describes DFF45. DFF40 is capable of inducing apoptosis, and may contain a nuclear localisation fragment. DFF45 acts as a molecular chaperone to direct the folding of DFF40. Although all DNase activity is associated with DFF40, DFF activity only occurs once DFF40 is complexed with DFF45. The DFF polypeptides and polynucleotides are useful for inhibiting the growth of cancer cells, and for inducing apoptosis of cells.
                                                                                                                                                                                                                                                                                                                                                        Sequence 2839
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                                                                                                TyrValSerAspIleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIle
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Human; DNA fragmentation factor; gene therapy; hyperproliferative psoriasis; angiogenesis; cancer;
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cytostatic; neoplasia; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying modulator of human DNA fragmentation factor 40, for treating cancer, involves contacting cell or cell-free composition comprising DFF40 with candidate substance and comparing apoptosis with
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06-JAN-1998;
22-AUG-1997;
22-AUG-1997;
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                                                                                                                                                                                       New isolated caspase activated nuclease which can inhibit or activate apoptosis heart attack, stroke or tumours
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P-PSDB; AAY04123.
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The present sequence encodes a caspase activated nuclease (CPAN). Active CPAN proteins can be used for identifying compounds which inhibit apoptosis. Inhibitors of apoptosis can be used therapeutically, e.g. where cells are damaged and the apoptotic pathway is initiated such as by heart attack or stroke. The inactive CPAN proteins can be used for

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                   The present sequence encodes a human DNA fragmentation factor, designated DFF40. Also described are: (1) a method of inducing apoptosis in a cell comprising providing the cell with DFF40 which results in apoptosis; (2) a method for inhibiting the growth of a cancer cell comprising contacting a cancer cell with a DNA fragmentation factor designated DFF40 under conditions permitting the uptake of the DNA cases conditions permitting the uptake of the DNA cases cell induces apoptosis; (3) a method for treating cancer comprising: (a) encoding a DFF40 DNA fragmentation factor; and (b) a promoter active in the tumour cell, where the promoter is operably linked to the region cencoding the DNA fragmentation factor, under conditions permitting the uptake of the nucleic acid by the tumour cell; (4) a method of identifying a modulator of DFF40; and (5) a method of producing a functional DNA fragmentation factor. An expression construct encoding a DNA fragmentation factor. An expression construct encoding a DNA fragmentation factor. An expression construct encoding a low of induce apoptosis, especially in tumour cells. DFF40 is used to inhibit the growth of a cancer cell, especially in humans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragmentation factor DFF40 nucleotide sequence.
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Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:

9.26e-174 1763.00 98.82% 98.82%

Length:
Matches:
Conservative:
Mismatches:

Query Match:

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US-09-748-451-2 (1-338) x AAZ38992 (1-2839)
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                                                                  LeuValHisIleValCysHisLysLysThrThrHisLysLeuAsnCysAspProSerArg 320
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                             IleTyrLysProGlnThrArgLeuLysArgLysGlnProValArgLysArgGln 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspLeuLeuHisAsnValSerGlnAsnIleAlaAlaGluThrArgAlaGluAspProPro 140
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                ATCTACAAACCCCAGACAAGGTTGAAGCGGAAGCAGCCTGTGCGGAAACGCCAG
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Best Local Similari
                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes an inhibitor (ICAD) for caspase-activating DNase (CAD). Two ICAD's are specifically claimed: a long chain form (ICAD-L) and a short chain form (ICAD-S). ICAD and ICAD can be used in the prevention of cell death, and can be used as a research reagent for cell death. The present sequence encodes mouse CAD which is used in the exemplification of the present invention.
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P-PSDB; AAY29931.
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                ProSerValProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGly 80
                                                     GluArgGlySerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPhe 60
                                                                                                          GTGGCGGCCCGGAGCTGCCAGGAGCTGCCTAAGGGCTGCGTTCCCAGCTCCCG
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/product= "CAD"
/note= "caspase-activating
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                                                                                                                      caspase activating DNase; CAD; inhibitor;
path; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                       GGAGGGAGGTGAACTGGGAGTACTTCTACAGCCTGCTCTTCACTGCCGAGAACCTGAAG
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/product= "CAD"
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DB; AAY29936.
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                             GluAlaGlnGluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgSerMet
                                                                     ValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuPro 40
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            GCAGCTCAAGAAGAGTACCTGCGAGTCCTTGGCTCCATGTGCCAGAAGCTCAAATCGGTG
                                                                                                                                                                                         GATCTTCTGCATCACGTGAGCCAGAATATTACTGCAGAGACCCGGGAGCAGGACCCATCC
                                                                                                                                                                                                          AspLeuLeuHisAsnValSerGlnAsnIleAlaAlaGluThrArgAlaGluAspProPro
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cancer

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RESULT 7
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ID AAI89481 standard; cDNA; 379 BE
XX AAI89481;
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DT 06-NOV-2001 (first entry)
XX
Human polynucleotide SEQ ID NO
DE Human; cytokine; cell prolifera
XW vaccine; peptide therapy; stem
XW tissue growth factor; immunomod
XW nervous system disorders; arthr
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PN W0200164835-A2.
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities,
                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
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                                                                                                                        Claim 1; SEQ ID NO 9541; 1399pp + Sequence Listing; English.
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P-PSDB; AAO09550.
                                                                                                                                                                                                                                                                             Tang YT,
                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                 28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001; 2001WO-US04927.
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                                                                                                                                                                                                                                                                               Liu C, Drmanac RT
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           Venter JC,
                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                  ABL15179 standard; cDNA; 1353
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                                                                                                                                                                 Drosophila melanogaster
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                                                         23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                           23-MAR-2001; 2001WO-US09231.
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                                 (PEKE ) PE CORP NY.
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89 GTGCGGAAACGACAG 75
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           Adams M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
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B; ABB71076.
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                                                                                                                                                                                                                                  GlnArg---GlnArgLeuLeuAlaAspLeuLeuHisAsnValSerGlnAsnIleAlaAla
                                                                                                                                                                                                                                                             CAATCGCCTTTGCTAAAGGTGGCT---GACATTTTCTACGATTTTATCGAACAGCATCCG
                                                                                                                                                                                                                                                                                                                                                                   GACGATGAGTACTTAAAAAGCCTACCC-----
                           LeuArg---
                                                                                                     GAGCGCTTCCACTCTAAGGAGGAAGCTATGGCCACACGTGCCCCAGACACGTGTGCGAGGC
                                                                                                                               SerArgPheGlnSerLysSerGlyTyrLeuArgTyrSerCysGluSerArgIleArgSer
                                                                                                                                                                                                           GAAAAGTTCCGCCGCATGATAACGGAGTATGAACACCAAAAGCAGCGACGCGTCCTGGAT 513
                                                                                                                                                                                                                                                                                                                                                                                          GluAsp---TyrPheProSerValProAspAsnAlaGluLeuValLeuThrLeuGly
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ACCCGCAATCCCTTGTACCGCCAAAATGCCAAGGCCCGACAAGTGATAAACTCTGTGCTG
                                                                           TyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGlnGluGluPhe
                                                                                                                                                        AACAGCAAGACCCACCTCAGCTTAAAGGCCGAGCACGTGGAGTGGTTCACGGGCGGCGAG
                                                                                                                                                                                    GluThr-
                                                                                                                                                                                                                                                                                     GlnValGlyLeuIleGlnAlaAlaGlnGlnLeuLeuCysAsp-----GluGlnAlaPro 113
                                                                                                                                                                                                                                                                                                                CCG-----GATGCAGTCATTACAACAGATGCCGATTTTGAGTTTGAGAAGATGCGACAA
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28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
03-APR-1998;
                       (CHIR )
(HYSE-)
                                                                                                                                                                                                                                              Human; gene; gene endetection; mapping; genetic analysis; co
                                                                                                                                                                                                                                                                                                Human gene expression product
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                                                                                                                                           28-JAN-1999;
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98US-0075954.
98US-0080114.
98US-0080515.
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    Crkvenjakov R, Dick
Escobedo J, Garcia
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apping; tissue typing; profiling; forensic; c
ysis; colorectal cancer; breast cancer; lung
    Dickson
arcia PD,
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M, Drmanac
Garcia V,
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        R, Drmanac
Giese K, I
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CC comprising the sequences given in AAZ12532 to AAZ1779. Also described is CC camerhod of detecting differentially expressed genes correlated with the CC cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels. CC mapping, tissue typing or profiling, forensics, genetic analysis and CC detection of polymorphisms. Polypertides encoded by the polynucleotide can be used for raising antibodies for experimental, diagnostic and CC therapeutic purposes. The polynucleotides may also be used to construct CC arrays for diagnostics (which may be used to determine function of an CC conced protein), and to detect differences in expression levels between coded protein, and to detect differences in expression levels between CC diagnostis, prognosis and management of odiseased tissue in a human, to CC cancer). The polynucleotides of the invention are especially used in the CC diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for CC peptide analogues and antagonists.
RESULT 10
ABL15178/c
ID ABL151
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Lamson G, Leshk
Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 735 BP; 141 A; 189 C;
                           ABL15178 standard; cDNA; 3758 BP
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                                                                                                                                                                                                                                                                                                                                                                      456 CTCCTGCACAACGTCANCCATAACATNGCGGACGAGACCNNGNCTGATGA-CCCCCGTGG
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                                                                                                                                                                                                                                                                                                            142 PheGluGlyLeuGluSerArgPheGlnSerLysSerGlyTyrLeuArgTyrSerCysGlu 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 GCCGNCCAGCANCTGCTGTGTGATGAGCAAGCCCCACAGAGGNANAAGCTGCTGGCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 AlaAlaGlnGlnLeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeuLeuAlaAsp 121
                                                                                                                                                                                                                                                                                     515 NTTGAAGC-TTGGAGTTNCGATTTCANAGCANGTNTGGCTATCTGANATACANCTGTNAG
                                                                                                                                                                                                                                                                                                                                                                                                                122 LeuLeuHisAsnValSerGlnAsnIleAlaAlaGluThrArgAlaGluAspProProTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 ValSerAspIleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGln 101
                                                                                                                                                                                                                       SerArgIleArgSerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGlu
                                                                                                                                                      AlaGlnGluGluPhe------LeuArgValLeuGlySerMetCys 194
                                                                                                                                                                                                AGCCGGATCCCGAGTTACCTGAGGGANGTGAGCTCCTA-CCNTCCACGGTGGGTGCGGAG
                                                                                                           NCTAA-GAGGAATTCTGCGGTCTTGCTCATTGCAGAGCTCCGTCATCATCATGC
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Leshkowitz D, Pot D, Randazzo F, Re
in B, Sudduth-Klinger J, Williams LT;
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303.50
68.64%
66.95%
16.96%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABJ16176-ABJ30511), expressed DNA sequences (ABJ16176-ABJ30511), expressed DNA sequences (ABJ16176-ABJ30511).
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3758
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 40016; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes from Drosophila interactions -
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genes from Drosophila and
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                    2122 TCCGACGATGAGTACTTAAAAAGCCTACCCGCCCAGACGCTGTTCATAGTGTCTGGCCCG 206
                                                                                                                        2176 ACCTTTTAGCTTCTCGAG-----CCACATTTGTATTTGGCTTCTGATGGCTTCGAGGTG 2123
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Similarity:
                                                                                                                                                     36 ArgPheGlnLeuProGluArgGlySerArgLeuCysLeuTyrGluAspGlyThrGluLeu 55
                                                                                        56 ThrGluAsp---TyrPheProSerValProAspAsnAlaGluLeuVal----
                                                                                                                                                                                                               16 ProArgLysPheGlyValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeu 35
                              -----LeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSer-----AspIle
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2000US-0614150
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                                                                                                         CGCCTACTGTGCTCCGACTGTCATGAGTATCGC 1049
                                                                                                                                                                                                 LeuLysLeuValHisIleValCysHisLysLys------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspSerCysLeuSerArgHisSerIleAsnProTyrSerAsnArgGluSerArgIleLeu 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATTCCTGAAGCAGCACTTGGGCGACGACGAAGAACAGACGCTGGCAGGATACCCAGCAAG 1499
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                                                                                                                                         LysLeuAsnCysAspProSerArgIleTyrLys 323
                                                                                                                                                                                                                                                  CAAGTGGTCGATATCTCAGTACTGGAGTACTTTCTAGAA---ATATTCTCCCTAAAGAAT 1142
                                                                                                                                                                                                                                                                          ArgGluValAsp-----TrpGluTyrPheTyrGlyLeuLeuPheThrSerGluAsn 298
                                                                                                                                                                                                                                                                                                                         GTTGCAAATGTGGAAGAACTTGTGAGTCATCCGCAGACCAAGTGTTCAATTCATAAGAAG 1199
                                                                                                                                                                                                                                                                                                                                                           ValGluAlaIleLysGlu-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGACTGAGGCAGGTGATTAGGGAGTACACCAAGGAAAACTGCATCCTCGACGAATGGTCC 1439
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                                                                                                                                                                            CTCAAACTAGTGCACATTGTCTGTCATGAGAAGGCGCAGCGCTCAAACCGTTCGAATGGT 1082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTCCTTGTGCTCCGACTTGGGTGACTTCTATTGCCAGGGCTCCTATTCGGAGAATGGC
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14-AUG-2002 (first entry)

differentially expressed in granulocytic cells #1334

adult respiratory distress syndrome; Crohn's disease; ulcerative colitis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosi cardiac reperfusion injury; renal reperfusion injury; ARDS; Human; ss; granulocytic cell; DNA chip; viral infection; parasitic infection; pufungal infection; sterile inflammatory of inflammatory bowel d periodontal disease; protozoal disease; psoriasis; bacterial infection; infection; thrombosis; bowel disease;

Homo sapiens.

WO200228999-A2

03-OCT-2001; 2001WO-US30821

03-OCT-2000; 2000US-237189P

(GENE-) GENE LOGIC INC

Beazer-Barclay Y, Weissman XX, Yamaga ß Vockley

WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and

Claim 1; SEQ ID No 1334; 114pp; English

CC GC, where differential expression of Gs is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent capable of modulating GCA or an inflammation (especially CC chronic) in a tissue, an allergic response in Gs: (2) screening (M3) CC chronic) in a tissue, an allergic response in a subject, exposure of a cubject to a pathogen or sterile inflammatory disease using the CC chronic) in a tissue, an allergic response in a subject, exposure of a cubject to a pathogen or sterile inflammatory disease using the CC chronic) in a tissue, an allergic response in a subject, exposure of a cubject to a pathogen or sterile inflammatory disease, by detecting the correct the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, or sterile inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for detecting a tissue having the detecting an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject capable of modulating GCA preferably in an inflammation in a tissue; M1 is useful for creening an agent that modulates the expression of gene(s) from GS in the tissue, an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, or a sterile continuation of disease (e.g. psoriasis, rheumatoid arthritis, creperfusion injury, renal processed in granulocytes.

CC parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present condition of the printed specification, but was obtained in electronic condition in the printed specification, but was obtained in electronic conditions. The present conditions are present c (GCA), by detecting the level of expression of gene(s) DNA chip analysis as given in the specification, and counter the expression level to an expression level in an unac-The invention relates to detecting (M1) granulocyte an unactivated and comparing (GC) (GS) identified уd

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Best Local Similarity:
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               1335 ---GAAGGCGAGGAGGAGTTTCTCTGCCTTTCCAAACTTTTCCTCCCTGAACCTG 139:
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                                                                                                                                                                                                                                                                                                                                                                                           144 GlyLeuGluSerArgPheGlnSerLysSerGlyTyrLeuArgTyr------
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                                        244 TyrSerAsnArgGluSerArgIleLeu------PheSerThr-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 ProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSer 83
                                                                                                  PheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHisSerIleAsnPro 243
                                                                                                                                                          GlySerTyrPheAspArgGlyAlaLysGlyGlySerArgLeuCysThrProGluGlyTrp
                                                                                                                                                                                                                                              GAAGAGAACTTTGCCGTTGAAGCTGCTAACTACCAAGACACTATTGGC----CGCCTGCAG
                                                                                                                                                                                                                                                                                                      TGTGAAGTGGATGCCCTTAAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATG 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProProTrpPhe-----Glu 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCGTGACGTACGTCAGCAATAT---GAAAGTGTGGCTGCCAAGAACCTGCAGGAGGCA 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuProGluArgGly 43
                                                                     CTCAATGTTAAGATGGCCCTTGACATTGAGATTGCCACCTACAGGAAGCTGCTG-----
                                                                                                                                                                                      GATGAGATTCAGAATATGAAGGAGGAAATGGCTCGTCACCTTCGTGAATACCAA----- 1274
                                                                                                                                                                                                                GluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgSerMetGlnTyrAsn 203
                                                                                                                                                                                                                                                                         -----SerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGln 183
                                                                                                                                                                                                                                                                                                                                   -----SerCysGluSerArgIleArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuAlaAspLeuLeuHisAsnValSerGlnAsnIleAlaAlaGluThrArgAlaGluAsp 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspIleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGlnAlaAla 103
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The present invention describes the full length genome of Neisseria meningitidis B (NNB). The Sequences in AAR721544 and AAF21607 to AAF721613 represent fragments of the NNB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each sequence by 49980 bp (1.e. the last 49980 bp of AAF21547 are repeated at the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of AAF21608, and so on). AAF721545 to AAF21588 encode the Neisseria proteins given in AAB58550 to AAB58553 and AAF21589 to AAF21606 represent PCR primers which are used in the exemplification of the present invention. The NNB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisseria nucleic acids, proteins and/or antibodies which binds to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Appendix A; 692pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis B full length genome sequence and frames are used to detect, treat and prevent Neisserial i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-647603/62.
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Galeotti C, Mora M,
Frazer CM, Grandi G;
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08-OCT-1999;
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(GENO-) INST GENOMIC RES
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99WO-US23573
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Ratti G, Scarselli M,
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Scarlato V,
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leAsnProTyrSerAsnArgGluSerArgIleLeuPheSerThrTrpAsnLeuAspHisI 261
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                                              -GCGCCAATA---CTTTCAGGTTGTCTTGAGCTTCGGCGCGCAA
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The present invention describes methods of obtaining immunogenic CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414 CC represent specifically claimed Neisseria meningitidis genomic DNA CC sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the claim of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the claim of Neisseria meningitidis DNA sequences; and AAA81321 to AAA81452 represent Neisseria meningitidis MAN polynucleotide ORF sequences, which are all used in the exemplification of the present composition. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences and/or against all pathogenic Neissariae. Identification of biological probes,
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                                                                                                                                                                                                                                                                                                              Claim 7; Page 866-1272; 1760pp;
                                                                                                                                                                                                                                                                                                                                             other Neisserial infections, for example,
                                                                                                                                                                                                                                                                                                                                                             Isolated nucleotide sequences of Neisseria used in the diagnosis and treatment of N. \mathbf{n}
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30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                GCGGAGCCTGCTCCACAACGACAGGCGCGCGGGTGCGGGTTCGGGTTCTGGCTCGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                          AATCCTTATCGAAACCGAACAGGGTTTTGGCAGACAGGGAAATGGTTTCATCAACATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AsnProTyrSerAsnArgGluSerArgIleLeuPheSerThrTrpAsnLeuAspHisIle 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TrpPheSerCysGlnGlyProPheAspMetAspSerCysLeuSer---ArgHisSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAACAGGTACGCCGTTGCTGACCAGGTTGTTTGCCACTACGTATGCGCGGCGTTCTGACA
                                                                                                                                                                                                                                                                IleLysGluGlnAspGlyArgGluValAspTrpGluTyrPheTyrGlyLeuLeuPheThr
                                                                                                                                                                                                                                                                                                                                                                                                           IleGlu------LysLysArgThrIleIleProThrLeuValGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GCGCCAATA---CTTTCAGGTTGTCTTGAGCTTCGGCGCGCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCCTGATTGTATTTGTCAGAACCCATAAAGTCGGTATGGCCTTCGACGCGGACAGATT 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGlnGluGluPhe---
                                                                                                                                                                                                      TTACGGTGTAACCCTGAACGGACGCCTCGCCCGCAACAGCAGTGCCGGAAGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGACATTGGTTCGACTCAGGCGTT----------
                                                                                  (first entry)
                                                     coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 A; 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SerMetCysGlnArg---
                                                                                                                                               DNA;
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105.00
37.88%
23.23%
5.87%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                           cytostatic,
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671

GTTGACAATGCGTCTCTGGCACGTCTTGACCCTTGAACGCAAAGTGGAATCTTTGCAAGAA 730

ProAspAsnAlaGluLeuValLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSer 83 ---AGGAGATGCTTCAGAGAGAG-GAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAT

64

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44

SerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPheProSerVal 63

670

614

615

603

AGAAATTGCAGG

24 ArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuProGluArgGly 43

4 LysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGly 23

AAGCCCGCGTCG----AGGTGGAGCGCGACAACCTGGCCGAGGACATCATGCGCCTCCGGG 601

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US-09-748-451-2 (1-338) x AAA09307
                           Query Match:
DB:
                                                       Best
                                                                                                                                          Percent Similarity:
                                                                                                Pred. No.:
                                                                                                             Alignment Scores:
                                                                                   Score:
                                                       Local Similarity:
                                                                                                                                                                                                     14-3-3epsilon, alpha-tropomyosin, vimentin, p0071, Ini-1, IP-1, IP-2, IP-3, IP-4, or IP-5. NIK1 (also referred to as Nek2) is a human homologue of the Aspergillus nidulans mitotic regulator, NIMA kinase. NIK1 is a serine/threonine-specific kinase and is thought to play a k role in cell-cycle events leading to the onset of mitosis. The complexes, their derivatives and NIK1 or NIK1-IP protein and DNA sequences, etc. are useful for treating or preventing a disease or disorder involving aberrant levels of the complex or protein. Such
                                                                                                                                                                                                                                                                                                                                 NIK1 protein as "bait". These are known sequences which encod interacting proteins. The invention concerns purified complex NLK1 protein and a NLK1 protein-interacting protein, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for treating cancer, neurodegenerative disorder, metabolic disorders
                                                                                                                                                                  metabolic
                                                                                                                                                                             disorders include cancer, hyperproliferative dineurodegenerative disorders, cardiomyopathies,
                                                                                                                                                                                                                                                                                                                                                                           AAA09303-09 were isolated in a modified yeast two hybrid
                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 142-145; 172pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nandabalan
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                                                                                                                                       Sequence 1766 BP; 479 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN
                                                                                                                                                                                                                                                                                                        Interacting protein is chosen from TrkA, protein phosphatase lalpha,
L4-3-3epsilon, alpha-tropomyosin, vimentin, p0071, Ini-1, IP-1, IP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                complex of a NLK1 protein and a NLK1 protein-interacting protein, ful for treating cancer, hyperproliferative disorder, rodegenerative disorder, cardiomyopathies, viral infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-303742/26
DB; AAY92335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                    disorders.
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                           1.4
102.50
34.42%
20.87%
5.73%
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                                                                                                                                       482 C;
                                                                                                                                                                                               hyperproliferative disorders
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 (1-1766)
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                                                                                                                                       449 G;
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                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                       356
                                                                                                                                       Η,
                                                                                                                                       0
                                                                                                                                                                                viral infections
                          1766
77
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128
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                                                                                                                                       other;
                                                                                                                                                                                                                                                                                                                                               complexes of
                                                                                                                                                                                                                                                                                                                                                               system using encode N1K1
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RESULT 16
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ID AAS94
XX AAS94
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                                                                                                                                                                                                                                       AAS94873 standard; DNA; 1939 BP
                           Human; foam cell differentiation; atherosclerosis; cerebral stroke; cardiovascular disorder; coronary artery disease; gene therapy; ds.
                                                                                          Human DNA sequence #128 expressed during foam cell differentiation
                                                                                                                                             14-FEB-2002
                                                                                                                                                                                            AAS94873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1085 GAAGAGAACTTTGCCGTTGAAGCTGCTAACTACCAAGACACTATTGGC----CGCCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1025 TGTGAAGTGGATGCCCTTAAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATG 108
                                                                                                                                                                                                                                                                                                                                 1484 GAATAAAAAAGAAATCCATATCTTA 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1142 GATGAGATTCAGAATATGAAGGAGGAAATGGCTCGTCACCTTCGTGAATACCAA----- 1195
                                                                                                                                                                                                                                                                                                                                                                                                                         1424 CATCACGATGACCTTGAATAAAATTGCACACTCAGTGCAGCAATATATTACCAGCAA 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 -----GlnGlnLeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeu 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 GlySerTyrPheAspArgGlyAlaLysGlyGlySerArgLeuCysThrProGluGlyTrp 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 GluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgSerMetGlnTyrAsn 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 -----SerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGln 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 965 GCCCTGCGCCAGGCAAAGCAGGAGTCCACTGAGTACCGGAGACAGGTGCAGTCCCTCACC 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 GlyLeuGluSerArgPheGlnSerLysSerGlyTyrLeuArgTyr------ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           905 GAAGAATGGTACAAATCCAAGTTTGCTGACCTCTCTGAGGCTGCCAACCGGAACAATGAC 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 ProproTrpPhe---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 LeuAlaAspLeuLeuHisAsnValSerGlnAsnIleAlaAlaGluThrArgAlaGluAsp 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    788 ATTCAGGAACAGCATGTCCAAATCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCC 847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 ProThrLeuValGluAlaIleLysGluGlnAspGlyArgGluValAsp------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 PheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHisSerIleAsnPro 243
                                                                                                                                                                                                                                                                                                                                                                             297 uAsnLeuLysLeuValHisIleVal 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 AspIleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGlnAlaAla 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCGTGACGTACGTCAGCAATAT --- GAAAGTGTGGCTGCCAAGAACCTGCAGGAGGCA 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCAATGTTAAGATGGCCCTTGACATTGAGATTGCCACCTACAGGAAGCTGCTG----- 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGAAACTAATCTGGATTCACTCCCTCTGGTTGATACCCACTCAAAAAGGACACTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TrpAsnLeuAspHisIle------IleGluLysLysArgThrIleIle 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrSerAsnArgGluSerArgIleLeu-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----CTGATTAAGACGGTTGAAACTAGAGATGGACAGGTTATCAACGAAACTTCTCAG 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GAAGGCGAGGAGCAGGATTTCTCTGCCTCTTCCAAACTTTTCCTCCCTGAACCTG 1312
                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TrpGluTyrPheTyrGlyLeuLeuPhe-ThrSerGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PheSerThr-----
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The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides are used in the diagnosis of disorders associated with foam cell development such as atheroscierosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotides gequences can also be used as PCR primers and probes. The polynucleotides of the invention are also useful in gene therapy. Ass94746-As95021 represent the human polynucleotide sequences of the invention which are differentially expressed during form cell differentianty expressed during form cell differentianty.
                                                                                                                                                                                                                                                                                                                                                                    Composition useful for diagnosis of conditions, disorders or diseases associated with atheroscierosis, comprises several polynucleotides that are differentially expressed in foam cell development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                Claim 1; Page 184-185; 315pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-010925/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shiffman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE GENOMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W0200177389-A2.
Sequence 1939 BP; 514 A; 551 C; 490 G; 383 T; 1 other;
                                   expressed during foam cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Somogyi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lawn R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porter GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mikita
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Percent Similarity: Best Local Similarity: Score: No.: 1.61 102.50 34.42% 20.87% 5.73% Mismatches: Conservative: 1939 77 50 128 115 16

Alignment Scores:

US-09-748-451-2 (1-338) x AAS94873 (1-1939)

Gaps:

Indels:

Query Match:

Дb	Q.	Ъ	Qу	Db	Qy	皮	Qy	장	VQ	Db	Qy
949	. 104	892	84	. 832	64	776	44	764	24	707	4
GATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCC	GlnGlnLeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeu 118	agaaactccacgaagaaggaaatccagga	AspīleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGlnAlaAla 103	8	64 ProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSer 83	776AGGAGATGCTTCAGAGAGAG-GAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAT 831	44 SerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPheProSerVal 63	764 AGAAATTGCAGG 775	24 ArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuProGluArgGly 43	cgrcgaggregagogogacaacotggoogaggacatoatgogoo	LysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGly 23
1008	18	148	.03	191	ຘ	131	ŭ	75	ù	63	ω̈.

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Porcine; acylglucos
N-acetylneuraminic
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122
AAT04122 standard; DNA;
                                                                                                                                                                                Porcine acylglucosamine-2-epimerase DNA
                                                                                                                                                                                                              09-MAY-1996 (first entry)
                  WO9526399-A1
                                                                                                           scrofa.
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                                                                                                                                    acylglucosamine-2-epimerase;
neuraminic acid; renin-binding
                                                                                                                                                                                                                                                                                                                                   GAATAAAAAAGAAATCCATATCTTA 1669
                                                                                                                                                                                                                                                                                                                                                                                               CATCACGATGACCTTGAATAAAAATTGCACACACTCAGTGCAGCAATATATTACCAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CTGATTAAGACGGTTGAAACTAGAGATGGACAGGTTATCAACGAAACTTCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProThrLeuValGluAlaIleLysGluGlnAspGlyArgGluValAsp------
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                                                                                                                                    renin-binding; enzymatic
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                                                                                                                                                                                                                                                                                                                                                                   305
                                                                                                                                                    N-acetylmannosamine;
                                                                                                                                    production;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT04122 encodes AAR79928 porcine acylglucosamine-2-epimerase with renin-binding activity. A2P can be used for the enzymatic prodn. of N-acetylmannosamine and N-acetylneuraminic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Pages 55-56; 74pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant acyl:glucosamine-2-epimerase with renin-binding - useful in enzymic production of N-acetyl:mannosamine and N-acetyl:neuraminic acid
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25-MAR-1994;
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DB; AAR79928.
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                                                                                                                                                                                                           aGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSerAspIleArgAr 87
                                                                                                                                                   CATGGCCATGAACGAGCTGTGGAGGGTGACGGCGGAGGCACGGTACCAGAGCGAAGCG--
                                                                                                                                                                             rArgAlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSerGl 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgLysGlyCysLeuArgPheGlnLeuProGluArgGlySerArg------LeuCy
                                                                                                                                                                                                                                                                                                                                                 CAAGTACGTCTGGCTGCAGGGGAGGCAGGTGTGGATG----TACTGTCGCCTGTACCG
 -PheLeuArgValLeu-GlySerMetCysGlnArgLeuArgSerMetGlnTyrAsnGlyS
                            GCTGGGCCGGCCCCAGCTCCCCGGGGCCGTGGCCTCGGAGTCCATGGCAGTGCCCATGAT
                                                                                                                  yTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSerSer--
                                                                                                                                                                                                                                                                                                 -----LeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeuLeuAlaAspLeuLe 123
                                                                                                                                                                                                                                                                                                                                CAAGCTTGAGCGCTTCCACCGCCCTGAG-----CTTCTGGATGCGGCTAAAGCAGGGGG
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                                                         -TyrProSerThrValGlyAlaGluAlaGlnGluGlu----
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            messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting RNAs from a piological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minitaring the detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minitaring the detecting RNA transcripts and splice variants of human or animal transcriptomes.
                                                                                                                                                                                                                                                                                                                                                      New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000;
02-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; mouse; r
splice variant;
                                                                                                                                                                                                                                                                                              Example 1; SEQ ID 24354; 47pp; English.
                                                                                                                                                                                                                                                                                                                                        developmental-specific genes
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to detect transcripts of a sub-transcriptome under a
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2001US-287724P
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t; transcriptome; oligonucleotide library; ss.
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
The present invention describes a method for examining ischaemic research invention describes a method for examining ischaemic research invention describes a method for examining ischaemic for a from comprising measuring the expression profile of a from (I). The method
                                                                                                                                      Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                          WPI; 2002-034733/04.
P-PSDB; ABB57310.
                                                                                                                                                                                                                                                         Ishikawa K, Asai S,
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                                                                                                                                                                                                                                                                                                                                                                                             22-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse ischaemic condition related cDNA sequence SEQ ID NO:866
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                                                                                                                                                                                                                                                                                            (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
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                                                                     PheAspArgGlyAlaLysGlyGlySerArgLeuCysThrProGluGlyTrpPheSerCys
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                                                                                                                                      LeuArgValLeuGlySerMetCysGlnArgLeuArgSerMetGlnTyrAsnGlySerTyr 206
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                                                                                            The invention relates to an isolated nucleic acid detection reagent
                                                                                                                    Claim 1; SEQ
                                                                                                                                                   New isolated nucleic acid
genes from Drosophila and
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                                                                                                                                                                                                                                                                                                                                                                                             biology; cell signalling; insecticide;
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                                                                                                                                                   detection reagent for detecting for elucidating cell signalling
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capable of detecting 1000 or more genes from Drosophila. The inventuesful in developmental biology and in elucidating cell signalling threations in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins

The invention

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The sequence data specification, but sequences (ABL0184) (ABB57737-ABB72072)

for this patent did not form twas obtained in electronic f

n part of the printed format directly from

WIPO

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pred. No.: 33.6
Score: 98.00
Percent Similarity: 34.048
Best Local Similarity: 19.158
Query Match: 5.488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2874 ATTTTCATTTCTCAAAGTGAACACCGCTTAATTGGATAGCTCATTTTATGTGTCCCTCCT 2815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2994 CATTGGATCGATGTGAGTAGCCCTTAAATAAAGGAAAAGGAAAACAGGCACTTAAAAAAT 2935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3054 GAGGAGTACTTTCGCACCCTCGACGAGAATACGGAACTGGTGGCCGTCTTTCCCGGAGAA 2995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2754 CATGGGACCAAAGCCAGGAAGATT------AAATTAAATGCTATCTGCACTCTGTTT 2704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2814 TTTATCTGCCATAATGACTAATTGCATTATTTCTTGAATGCCATGAAAGAGCTCCATGAG 2755
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                                                                                                             2421 TTAATTCCTTTCCCATATACCACTTAATTGTAGCATGATTTCATGACTTTTAGGCCATTGT 2362
                                                                                                                                                                                                                          2481 GTTGGTGGACATCACGGGAAAGGAGTTTATGGAGCAGCTCAAGGATGCGGGAAGGTGAGT 2422
                                                                                                                                                                                                                                                                                                                                          2361 GTGCCAAGCGGAATG-------------CCGAGGATCGTTTAAATCTGCTGAAGCTAT 2317
                                                                                                                                                                                                                                                                        204 ---GlySerTyrPheAspArgGlyAlaLysGlyGlySerArg------ 216
                                                                                                                                                                                                                                                                                                                                                                               187 LeuArgValLeuGlySerMetCysGlnArgLeuArgSerMetGlnTyrAsn----- 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 TyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGlnGluGluPhe 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 AlaAlaGluThrArgAlaGluAsp-----ProProTrpPheGluGly-----LeuGlu 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 GlnAlaProGlnArgGlnArgLeuLeuAlaAspLeuLeuHisAsnValSerGlnAsnIle 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 LeuLeuCys------AspGlu 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 GluAspTyrPheProSerValProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGln 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 GlnLeuProGluArgGlySerArgLeuCysLeuTyrGluAspGlyThrGluLeu---Thr 56
                                                 219 ThrProGluGlyTrpPheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArg 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 GlyTyrValSer-----AspIleArg 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 ArgPheLeuSerAlaPheHisGluProGlnValGly---LeuIleGlnAlaAlaGlnGln 105
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Matches:
Conservative:
Mismatches:
Indels:
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Search completed: May 26, 2003, 16:31:19
Job time : 729 secs

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Command line parameters:

-MODEL-framet_P2n.model -DEV-x1h
-O-/cgn2_1/USFTO_spool/US09748451/runat_21052003_153830_16303/app_query.fasta_1.519
-O-/cgn2_1/USFTO_spool/US09748451/runat_21052003_153830_16303/app_query.fasta_1.519
-DB-Issued_Patents_NA -OPMT-fastap -SUFFIX-rn1 -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATKIX-blosum62 -TRANS-human40.cd1
-LIST-45 -DCCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MO- -ALIGN-20
-NODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-NODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US09748451_eCGN_1_1_40_erunat_21052003_153830_15303 -NOPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT=30 -THREADS-1 -XGAPOP-10 -XGAPEXT=0.5 -FGAPOP-6
-FGAPEXT=7 -YGAPOP-10 -YGAPEXT=0.5 -DELOP-6 -DELEXT-7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                1789
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-061-702-1
US-08-53-703A-5
US-08-53-703A-9
US-09-006-021-9
US-09-006-021-9
US-07-938-782A-1
PCT-US-30-524-1
PCT-US-30-08131-1
US-09-069-023-21
US-09-065-193B-8
US-09-061-702-3
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1645.345 Million cell updates/sec
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Sequence
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4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.8	4.8	4.8	4 .8	4.8	4.8	4.9	4.9	4.9	4.9
10163	10163	3168	3168	3168	2268	2268	4411529	4403765	2680	2680	20235	20235	4287	4287	15108	15108	15108	15101	15101	4201	1124	507	1155	1155	4411529	4403765	1114	4322	2637	2637	1049	9633
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ALIGNMENTS

RESULT 1 US-09-061-702-1

sequence 1, Application US/09061702
Patent No. 6165737

INFORMATION:

APPLICANT: Wang, Xisodong
APPLICANT: Liu, Xuesong
TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN
TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN
TITLE OF INVENTION: APOPTOSIS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS: 21

CORRESPONDENCE ADDRESS: 21

CORRESPONDENCE ADDRESS: 21

COUNTRY: USA
ZIP: 77210-4433

COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER PATON Release #1.0, Version #1.30

CURRENT APPLICATION PATA:
APPLICATION NUMBER: US/09/061,702
FILING DATE: CONCURTENTY
APPLICATION HORDATION:
ARTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US/09/061,702
FILING DATE: CONCURTENTY
ARE MCM1111an, Nabeela R.
REGISTRATION NUMBER: US/09/061,703

REFERENCE/DOCKET NUMBER: US/09/061,703

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DB:
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Best Local Similarity:
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                  IleIleGluLysLysArgThrIleIleProThrLeuValGluAlaIleLysGluGlnAsp 280
                                                                                         IleAsnProTyrSerAsnArgGluSerArgIleLeuPheSerThrTrpAsnLeuAspHis
                                                                                                                       GlnAlaAlaGlnGlnLeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeuLeuAla 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyArgGluValAspTrpGluTyrPheTyrGlyLeuLeuPheThrSerGluAsnLeuLys
                                                                                                                                                                                                                                                                                                                 TrpPheGluGlyLeuGluSerArgPheGlnSerLysSerGlyTyrLeuArgTyrSerCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetLeuGlnLysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGly ·20
                                                                            ATCAACCCCTACAGTAACAGGGAGAGCAGGATCCTCTTCAGCACCTGGAACCTGGATCAC
                                                                                                                                                                                                                                                                                                      TGGTTTGAAGGCTTGGAGTCCCGATTTCAGAGCAAGTCTGGCTATCTGAGATACAGCTGT
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US-08-553-703A-5
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                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Applic Patent No. 5795767
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION UMBER:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
ALLman, DANIel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714,760-0404
                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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APPLICANT: OHTA, YASUHIRO
APPLICANT: TSUKADA, YOJI
TITLE OF INVENTION: EPIMERASE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                               LENGTH: 1209 base pai
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 30-NO
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SOFTWARE: FastSE(
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COMPUTER: II
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                                                      IleTyrLysProGlnThrArgLeuLysArgLysGlnProValArgLysArgGln 338
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                          sLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPheProSerValProAspAsnAl
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101.50
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Indels:
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RESULT 3
US-08-553-703A-9
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GENERAL INFORMATION:
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                                                                                                                                               NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                       ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                     APPLICANT: MARU, ISAFUMI
APPLICANT: OHTA, YASUHIRO
APPLICANT: TSUKADA, YOJI
                                                                                                                                                                                                                                                                           TTLE OF INVENTION: EPIMERASE
     COMPUTER: IBM Compatible
                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             846 CTCCGGATGGGACGCTGATCAC 867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       492 GCTGGGCCGGCCCCAGCTCCCCGGGGCCGTGGCCTCGGAGTCCATGGCAGTGCCCATGAT 551
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Best Local Similarity:
Query Match:
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US-08-553-703A-9
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SOFTWARE: FASTSEO VETSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,703A
FILING DATE: 30-NOV-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1209 base pair
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
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LOCATION: 1...1206
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REGISTRATION NUMBER: 34,115
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174 -----TyrProSerThrValGlyAlaGluAlaGlnGluGlu----
                                                442 -----GTGGACATGATGGATCAGATCGTGCACTGGGTGCGAGAGGACCCCTCTGG 491
                                                                                            154 yTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSerSer-- 173
                                                                                                                                               384 CATGGCCATGAACGAGCTGTGGAGGGTGACGGCGGGGGCACGGTACCAGAGCGAAGCG-- 441
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-006-021-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                    TOPOLOGY: 1:
MOLECULE TYPE:
-09-006-021-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006.
                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/5
FILING DATE: 30-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 714-760-0404
                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MARU, ISAFUMI
APPLICANT: OHTA, YASUHIRO
APPLICANT: TSUKADA, YOJI
TITLE OF INVENTION: EPIMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER OF SEQUENCES:
                                                              STRANDEDNESS:
                                                                                                                                                  TELEFAX: 714-760-9502
                                                                                                                                                                                                      NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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GENERAL I
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SEQUENCE CHARACTERISTICS:
LENGTH: 1209 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/553,703
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TSUKADA, YOJI
TITLE OF INVENTION: EPIMERASE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MARU, ISAFUMI
APPLICANT: OHTA, YASUHIRO
APPLICANT: TSUKADA, YOJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ment Scores:
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FILING DATE: 30-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Allman, Daniel E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No..
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CITY: Newport Beach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Coding Sequence LOCATION: 1...1206
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                                                           87 gPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGlnAlaAlaGlnGln---- 105
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Matches:
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US-07-938-782A-1
; Sequence 1, Application US/07938782A
; Patent No. 5525513
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                                                      ZIF: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/938,782A
FILING DATE: 31-NG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: London, Irving M.
TITLE OF INVENTION: DNA Encoding the Heme-Regulated
TITLE OF INVENTION: Eurkaryotic Initiation Factor 2 alpha kinase
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STARE
                                       CLASSIFICATION:
                                                                                                                                                                                                                              COUNTRY: US
ZIP: 30309-3450
                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 yTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSerSer-- 173
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Y: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen, Jane J.
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Percent Similarity:
Best Local Similarity:
                                                                                                                                                           US-07-938-782A-1
 US-09-748-451-2 (1-338)
                                                                                                                           Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                              PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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NAME/KEY:
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ORIGINAL SOURCE:
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LOCATION: 1009..1031
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                  AUTHORS:
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September-1991
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regulated eukaryotic initiation factor
Zalpha (eIF-Zalpha)kinase of rabbit reticulocytes:
Homology to yeast GCN2 protein kinase and human
double-stranded-RNA-dependent
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x US-07-938-782A-1 (1-2729)
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35.43%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Expression of HRI mRNA in Human erythroid cells, using as the probe rabbit HRI cDNA from nucleotides 113 to 2149."
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amplification of human HRI cDNA sec
using the rabbit HRI cDNA sequence
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amplification of human HRI cDNA sec
using the rabbit HRI cDNA sequence.
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Conservative:
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                                                                                        Sequence 1, Application Patent No. 5690930 GENERAL INFORMATION:
APPLICANT: Chen, Jane J.
APPLICANT: London, Irving M.
APPLICANT: INVENTION: DNA Enco-
TITLE OF INVENTION: Eurkaryo
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                                                                                                                                                                                                                                                                                                                                                                     IleLeuPheSerThrTrpAsnLeuAspHisIleIleGluLysLysArgThrIleIlePro 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGATCGGAGTATGATGCCAAGTCAGACATGTACAGCGTCGGCGTGATCCTGCTGGAGCTC 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspMetAspSerCysLeuSerArgHisSerIleAsnProTyrSerAsnArgGluSerArg 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerMetGlnTyrAsnGlySerTyrPheAspArgGlyAlaLysGlyGly--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCTCCCTGCCTAGCCGTCACTCGGCCACGTCACAGGGGAACGTGGACTTGCACTTGCA 2038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGCGAGCTGGCCGCATACCCGACTCCCTCAGTAAGAGGTGCCCGGCGCAGGCCAAGTAC 1774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGly
                                                                                                                                           Application US/08630524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAATCACTCAGCCCGCATGACTCTCCCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGTCAACTGGAATGGACAATTTCAAGCCTCCTGAGGTTCAGGCGGCATAATCCTCACT 2098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProSerThrValGlyAlaGluAlaGlnGluGluPheLeuArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSerSerTyr 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgAlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSerGly 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProGlnValGlyLeuIleGlnAlaAlaGlnGlnLeuLeuCysAspGluGlnAlaProGln 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyGlnAlaTrpGlnGlyTyrValSerAspIleArgArgPheLeuSerAlaPheHisGlu 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluAspTyrPheProSerValProAsp-----AsnAlaGluLeuValLeuLeuThrLeu 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuProGluArgGlySerArgLeu-----CysLeuTyrGluAspGlyThrGluLeuThr 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGCCTAGAAATATTTTTCTTCATGGTCCTGATCAACAAGTGAAAATAGGAGACTTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----TTCCAGCCCTTCGGGACAGAGATGGAGCGG---GCAGAGGTCCTGACGGGC 1714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SerArgLeuCysThrProGluGlyTrpPheSerCysGlnGlyProPhe 230
DNA Encoding the Heme-Regulated Eurkaryotic Initiation Factor 2
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  alpha kinase
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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCES_TOOKKET NUMBER: WU10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8795
TELEPAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: 543.560
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: amplification of human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 448.468
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: amplification of human HRI cDNA sequence."
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1009.1031
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: using the rabbit HRI cDNA sequence.
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 31-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Date: Date: 1
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CORRESPONDENCE ADDRESS:
CADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 113. 2149
OTHER INFORMATION: /note= "Expression of HRI
OTHER INFORMATION: mRNA in Human erythroid cells, using as
OTHER INFORMATION: probe rabbit HRI cDNA from nucleotides
OTHER INFORMATION: to 2149."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/01 FILING DATE: 10-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
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: Georgia
RY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reticulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA
                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Primer used in the amplification of human HRI cDNA sequence using the rabbit HRI cDNA sequence."
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                             HRI cDNA sequence
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Best Local Similarity:
Query Match:
DB:
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TITLE:
TITLE:
TITLE:
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PAGES: 7729-7733
DATE: September-1991
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                                                                                                                                                                1979 GAGCTCCCTGCCTAGCCGTCACTCGGCCACGTCACAGGGGAACGTGGACTTGCACTTGCA 2038
                                                                      2039 GCAGTCAACTGGAATGGACAATTTCAAGCCTCCTGAGGTTCAGGCGGCATAATCCTCACT 2098
                                                                                                                                                                                                                                                          1919 AAGAAGCAGCTGAGCCTCCTCCCCAGGCCCGAGGGGTGAGGAGTGACAGGCGAGACGGA 1978
                                                                                                                                                                                                                                                                                                                                                    1859 CATGTTAACCTCACCCTACAGATGAAGATAATAGAGCAGGAAAGAGAAATCGAGGAACTC 1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1547 GCACCCACACACTTCCCGAGTGGGCACCTGTCTGTACGCCTCGCCCGAGCAGTTGGAA 1606
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                                                                                                               199 SerMetGlnTyrAsnGlySerTyrPheAspArgGlyAlaLysGlyGly------
                                                                                                                                                                                                                                                                                                      175 ProSerThrValGlyAlaGluAlaGlnGluGluPheLeuArg------ 188
                                                                                                                                                                                                                                                                                                                                                                                                155 TyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSerSerTyr 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 ArgAlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSerGly 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 ArgGlnArgLeuLeuAlaAspLeuLeuHisAsnValSerGlnAsnIleAlaAlaGluThr 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 ProGlnValGlyLeuIleGlnAlaAlaGlnGlnLeuLeuCysAspGluGlnAlaProGln 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 GlyGlnAlaTrpGlnGlyTyrValSerAspIleArgArgPheLeuSerAlaPheHisGlu 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 GluAspTyrPheProSerValProAsp-----AsnAlaGluLeuValLeuLeuThrLeu 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 LeuProGluArgGlySerArgLeu-----CysLeuTyrGluAspGlyThrGluLeuThr 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 ArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPhe------Gln 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGly
                                                                                                                                                                                                            -----ValLeuGlySerMetCysGlnArgLeuArg 198
                                                                                                                                                                                                                                                                                                                                                                                                                                              ------CCGTCCGCCCTTCAGCTGCTGCAGAGTGAGCTCTTCCAGAACTCCGCG 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S: London, Irving M.

Cloning of the CDNA of the heme-
regulated eukaryotic initiation factor
regulated eukaryotic initiation factor
2alpha (eIF-2alpha)kinase of rabbit reticulocytes:
46mology to yeast GCN2 protein kinase and human
double-stranded-RNA-dependent
couble-stranded-RNA-dependent
reproc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen, Jane J
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96.00
35.43%
20.53%
5.37%
SerArgLeuCysThrProGluGlyTrpPheSerCysGlnGlyProPhe 230 :::|||:::
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Matches:
Conservative:
Mismatches:
Indels:
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PCT-US93-08131-1
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    NEORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Massachusetts Institute Of Technology
TITLE OF INVENTION: DNA Encoding the Heme-Regulated
TITLE OF INVENTION: Eukaryotic Initiation Factor 2 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                        FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                               EATURE:
                                                                                              EATURE:
                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
 NAME/KEY:
                                                              NAME/KEY:
                                              OTHER INFORMATION:
                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                         ORGANISM:
CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Pabst, Patrea REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                           NAME/KEY:
                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                             LOCATION:
                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US93/08131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 21
LENGTH: 2143
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APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
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Patent No. 6348573
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SEQ ID NO 19
LENUTH: 1167
TYPE: DNA
ORGANISM: Mus musculus
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US-09-069-023-19
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                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
US-09-748-451-2 (1-338) x US-09-069-023-19 (1-1167)
                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                        US-09-069-023-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inchara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/09069023A Patent No. 6348573
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                 No : :
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Matches:
Conservative:
Mismatches:
Indels:
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RESULT
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                 ATTORNEY/AGENT INFORMATION:
NAME: LAISON, MAILIR T.
REGISTRATION UNDBER: 3238
REFERENCE/DOCKET NUMBER: UBC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
TELEPAX: (970) 668-2052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kalchman,
TITLE OF INVENTION: A
TITLE OF INVENTION: H
NUMBER OF SEQUENCES:
                                                                                                                                                                                   OPERATING SYSTEM: MS D
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
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                                                                                                                                                                                                                                                                                                                  CITY: Frisco
STATE: CO
                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                   RRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        COUNTRY:
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PO Box 5270
                                                                                                                                                                                                                                                                                                        USA
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Huq, A.H.M. Mahbubul
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     ID NO:
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Best Local Similarity:
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OTHER INFORMATION:
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LENGTH: 2301
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HYPOTHETICAL:
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TOPOLOGY: linear
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                                                               TrpPheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHisSerIleAsn
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Score: 89.00 Matches: 78 Percent Similarity: 36.18% Conservative: 49 Best Local Similarity: 22.22% Mismatches: 146 Query Match: 4.97% Indels: 78	LOCATION: 1131105 161-702-3 ent Scores: 0.814 Length:	ESS: line	5 LE 5	57 57	ON: INFORMATION: 11an, Nabeela F	; SOFTWARE: PatentIn Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/061,702 FILING DATE: Concurrently Herewith	ATUR	h 433	R OF SEQUENCES: SPONDENCE ADDRES RESSEE: Arnold, BET: P.O. Box 4	; APPLICANT: Wang, Xiaodong ; APPLICANT: Liu, Xuesong ; TITLE OF INVENTION: DAN FRAGMENTATION FACTOR INVOLVED IN ; TITLE OF INVENTION: APOPTOSIS	RESULT 12 US-09-061-702-3 ; Sequence 3, Application US/09061702 ; Patent No. 6165737 ; Patent No. 616737		TIGACCGGTGACACTGTCATCCAGGGGAGTGCCACCAGCCTCCGGGCCCACCGGAGCCA	1190 TARCTGGCCCAGAAGATATTAGTGAGCTTCTGCACTCGATCACCCTGCTTGCCCAC	1187 CAG		Db 1082CTTGAGGAACCCACCCTCATCAGCAGGATCCACAGATCACCTTCTC 1132 Oy 263 GluLysLysArgThrIleIleProThrLeuValGluAlaIleLysGluGlnAspGlyArg 282
917 AAAGCACTGGCTGTTGCCTTGAACTGGGACATAAAGAAGACGGAGACTGTTCAGGAGGCC 328 LeuLysargLysGlnProValArgLysargGln 338	Qy 288 TyrPheTyrGlyLeuLeuPheThrSerGluAsnLeuLysLeuValHislleValCysHis 307 Db 869CTGAGCTTATCTACTAGCATTTGGAGTTGCAAGGAAGAAGACCCC 916	Qy 268 IleTleProThrLeuValGluAlaIleLysGluGlnAspGlyArgGluValAspTrpGlu 287	Qy 248 GluSerArgIleLeuPheSerThrTrpAsnLeuAspHisIleIleGluLysLysArgThr 267	QY 232	Qy 213 GlyGlySerArgLeuCysThrProGluGlyTrpPheSerCysGlnGlyProPheAsp 231	Qy 193 MetCysGlnArgLeuArgSerMetGlnTyrAsnGlySerTyrPheAspArgGlyAlaLys 212	Qy 173 SerTyrProSerThrValGlyAlaGluAlaGluGluPheLeuArgValLeuGlySer 192 :::	Qy 153 SerGlyTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSer 172	Qy 133 GluThrargAlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLys 152	Qy 113 ProGlnArgGlnArgLeuLeuAlaAspLeuLeuHisAsnValSerGlnAsnIleAlaAla 132	. eulleGlnAlaAlaGlnGlnLeuLeuCysAspGluGlnAla ::: ::: ::::: CAGCTTGGATTTCCCAAGAGTCCTTTGATGTAGATGAAACA	Oy 73 ThrLeuGlyGlnAlaTrpGlnGlyTyrValSerAspIleArgArgPheLeuSerAlaPhe 92 Db 377 GCTAGTAATGAGAAATGG	Qy 54 GluLeuThrGluAspTyrPheProSerValProAspAsnAlaGluLeuValLeuLeu 72 ::: ::: Db 317 ATAGTGGATGATGACGATTACTTTCTGTGTCTACTTCCAATACTATGTGTGGCATTC 376	Qy 35LeuArgPheGlnLeuProGluArgGlySerArgLeuCysLeuTyrGluAspGlyThr 53	Qy 17 ArgLysPheGlyValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCys 34 :::	Qy 5 ProLysSerValLysLeuArgAlaLeuArgSerPro 16 ::: ::::: :::	DB: 4 Gaps: 15 US-09-748-451-2 (1-338) x US-09-061-702-3 (1-1689)

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                                     GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: SCHOOLSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SCHOALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
                                                                                                                                                                      Sequence 13, Application US/09069023A Patent No. 6348573
   CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27
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CURRENT APPLICATION NUMBER: US
APPLICATION NUMBER: US
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Local Similarity:
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                             Sequence 1, Application US/08794158 Patent No. 6387655
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SOFTWARE: PatentIn Ver
SEQ ID NO 13
                                                                                                             GENERAL INFORMATION:
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             APPLICANT: Burnett Jr., J.
APPLICANT: Mayne, Nancy G.
APPLICANT: Sharp, Robert L.
TITLE OF INVENTION: Excitat
TITLE OF INVENTION: and Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372 GAAAAAGGACAGAAGTGGATGCCGGGCAGCCAGCACGTCCC-CACTTGCTCGCCGCCGAA 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 CysLeuArgPheGlnLeuProGluArgGlySerArgLeuCysLeuTyrGluAspGlyThr 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrLeuGlyGlnAlaTrpGlnGlyTyrValSerAspIleArgArgPheLeuSerAlaPhe
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                                                                                                                                                                                                                                                                                                   GGTGCTGGATGACAAGGAAGAGCGGCCATCCCTCCGGTCACAAGCCAAGGGCAGGTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                              uArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGlnGluGluPheLeuAr
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             Excitatory Amino Acid Receptor Protein and Related Nucleic Acid Compounds
and Related
3
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Indels:
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COUNTRY:

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US-09-748-451-2 (1-338) x US-08-794-158-1 (1-2637)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/08/704 ""

FILING DATE:
CLASSTO. PACE OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Lilly Corpo
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 39,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                  554 ATTACTTTGCCAGGACCGTGCCCCC-----CGACTTCTACCAGGCCAAAGCCATGG 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 nLeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeuLeuAlaAspLeuLeuHis-- 124
                                                                      146 uSerArgPheGlnSerLysSerGlyTyrLeuArgTyrSerCysGluSerArgIleArgSe 166
                                                                                                                                                                                                                                                                                                    605 CTGAGATCTTGCGCTTCTTCAACTGGACCTACGTGTCCACAGTAGCCTCCGAGGGTGATT 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         494 AGATCCCTCAGATCAGCTACGCATCCACCAGCGCCAAACTCAGTGATAAGTCGCGCTATG 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 TCATTGGTGGCTCTTATAGCAGTGTTTCCATACAGGTGGCAAACCTGCTGCGGCTCTTCC 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 ArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGlnAla-AlaGlnGl 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 AsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSerAspIle 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 LeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPheProSerValProAsp 65
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T---CGCTACGGCGGAGAAGGTGGGCCGCTCCAACATCCGCAAGTCCTACGACAGCGTGA 778
                                                                                                                                                                                                                                                                                                                                                                           ACGGGGAGACAGGATCGAGGCCTTCGAGCAGGAAGCCCCGCCT---GCGCAACATCTGCA 721
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22.12%
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 16
US-08-794-158-3
; Sequence 3, Ap
; Patent No. 638
; GENERAL INFOR
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                                                                                                                                                                    COUNTRY: U.S..

ZIP: 46285
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,158
FILING DATE:
CLASSIFICATION: 435
APTODENCY ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08794158 Patent No. 6387655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                          ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Burnett Jr., J. Paul
APPLICANT: Mayne, Nancy G.
APPLICANT: Sharp, Robert L.
TITLE OF INVENTION: Excitatory Amino Acid Receptor Protein
TITLE OF INVENTION: and Related Nucleic Acid Compounds
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: El1 Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1154 AGCAAGAGTCCAAGATCATGTTTGTGGTGAACGCGGTGTATGCCATGGCCCACGCTTTGC 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1274 TGGATGGGAAGAAGTTGTACAAGGATTACTTGCTGAAAATCAACTTCACGGCT 1326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 luLys---LysArgThrIleIleProThr------LeuValGluAlaIleLysGluG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 lnAspGlyArgGluValAspTrpGluTyrPheTyrGlyLeuLeuPheThrSer 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  932 AGGGCAGCGATGTGGCCTACGGCGCCATCACCCTGGAGCCTGCCCCAGCCTGTCC 991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         872 CCAATGCCTCCTTCACCTGGGTGGCCAGCGACGGCTGGGGCGCGCAGGAGGAGCATCATCA 931
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                                   x-9962
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Percent Similarity: Best Local Similarity:

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Alignment Scores:

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MOLECULE TYPE: ANTI-SENSE: HYPOTHETICAL:

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US-08-794-158-3
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2637 base pairs
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No.:
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HYPOTHETICAL: NO
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1034 ACCACCGCAACCCCUGGUUCCGGGACUUCUGGGAGCAAAAGUUUCAGUGCAGCCUCCAGA 1093
                                      246
                                                                          992
                                                                                                                                                932
                                                                                                      228 yPro-PheAspMetAspSerCysLeuSerArgHis-----SerTleAsnProTyrSerA 246
                                                                                                                                                                                  214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 uSerArgPheGlnSerLysSerGlyTyrLeuArgTyrSerCysGluSerArgIleArgSe 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       665 ACGGGGAGACAGGGAUCGAGGCCUUCGAGCAGGAAGCCCGCCU---GCGCAACAUCUGCA 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  554 AUUACUUUGCCAGGACCGUGCCCCC------CGACUUCUACCAGGCCAAAGCCAUGG 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
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                                                                                                                                            AGGGCAGCGAGCAÜGÜGGCCUACGGCGCCAUCACCCÜGGAGCCÜGCCCAGCCUGUCC
                                                                                                                                                                                                                                                 uArgSerMetGlnTyrAsnGlySerTyrPheAspArgGlyAlaLysGly----- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nLeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeuLeuAlaAspLeuLeuHis-- 124
                                        Sn-------
                                                                        GCCAGUUCGAC------CGCUACUUCCAGAGCCUCAACCCCUACAACA 1033
                                                                                                                                                                              -GlySerArgLeuCys------ThrProGluGlyTrpPheSerCysGlnGl 228
                                                                                                                                                                                                                 CCAAUGCCUCCUUCACCUGGGUGGCCAGCGACGGCUGGGGCGCGCAGGAGAGCAUCAUCA 931
                                                                                                                                                                                                                                                                                        UCGUGGUCCUCUUCAUGCGCAGCGACGACUCGCGGGAGCUCAUUGCAGCCGCCAGCCGCG 871
                                                                                                                                                                                                                                                                                                                         -----GluGluPheLeuArgValLeuGlySerMetCysGlnArg-----Le 197
                                                                                                                                                                                                                                                                                                                                                                                                                                   U----CGCUACGGCGGAGAAGGUGGGCCGCUCCAACAUCCGCAAGUCCUACGACAGCGUGA 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUGAGAUCUUGCGCUUCUUCAACUGGACCUACGUGUCCACAGUAGCCUCCGAGGGUGAUU 664
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Matches:
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Db .	us-09-	Alignment Pred. No. Score: Percent S Best Loca Query Mat DB:	INFO SE	A:		QZHHA	RESULT 17 US-08-537- Sequence Patent No. GENERAL APPLIA	ob Db	Db .	Qу	Qу
5 P 1 1364 C	748-451-2	No.: No.: Int Similarity: Local Similarity:	LECOMMU TELEPHO TELEFAX RMATION QUENCE LENGTH: TYPE: STRANDE TOPOLOG LECULE 37-342-	APPLICATION NUMBER: US/O FILING DATE: 02-OCT-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: A9r1s, Dr. Cheryl REGISTRATION NUMBER: 34 REFERENCE/DCCKET NUMBER: 34	COUNTRY: United 21P: 10174-640, 21P: 10174-640, COMPUTER READABLE MEDIUM TYPE: F COMPUTER: IBM OPERATING SYSTEL SOFTWARE: Pate CURRENT APPLICATION	APPLICANT: BAI TITLE OF INVENI TITLE OF INVENI NUMBER OF SEQUI CORRESPONDENCE ADDRESSEE: 1 STREET: 405 CITY: New Yo	342- 1, INF	279 1 1274 U	263 l	247 - 1154 A	246 - 1094 A
ProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGl	(1-338)	s: ity: larity:	NICATION INI NE: 212-86: : 212-878-: : 218-878-: : FOR SEQ ID CHARACTERIS' 4322 base nucleic acid DNESS: sine Y: linear Y: linear TYPE: DNA	APPLICATION NUMBER: US/ FILING DATE: 02-0CT-199 CLASSIFICATION: 435 TORNEY/AGENT INFORMATION NAME: Agris, Dr. Cheryl REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:	COUNTRY: United States of Americ ZIF: 10174-5401 MPUTER READABLE FORM: MEDIIM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, IRRENT APPLICATION DATA:	HADDENTION NVENTION NVENTION NVENTION SEQUENCE ADDENCE ADDENCE: No. E: No. 405 Lex New York	44 p	nAspGlyA : GGAUGGGA	luLysL : ACAAAAUGC	-ArgGluS ::: GCAAGAGU	CAAACGCA
ValLysLe ::: GATCAACT	×	7.49 86.50 33.41% 20.49% 4.84%	v INFORMATIO 7-867-0123 378-9655 3 ID NO: 1: EXISTICS: ase pairs acid single sar ax (genomic	UMBER: US/08/53 02-OCT-1995 NR: 435 INFORMATION: Dr. Cheryl H. Dr. Cheryl H. NUMBER: 34,086 KET NUMBER: 427	ed States o 01 01 E FORM: Floppy disk PC compati PC -DOS EM: PC -DOS entIn Relea	Lars Muta 1 G- : 7 ESS: 840486	on US/08	rgGluVal ::::::: AGAAGUUG	-LysArgThrIleIleProThr ::: ::: GCAGCGCACCCUCUGUCCCAACACUAC	erArgIle ::: CCAAGAUC	ACCACAGG
uArgAlaL AATGGCAG	US-08-537-342-1		1:	US/08/537,342 1995 ION: IV) H. 34,086 34,086 ER: 4276.050-US	of Americ k ible is/MS-DOS	t DNA	US/08537342	AspTrpG1 :: UACAAGGA	IleIlePr :::	LeuPhe ::: Auguuugu	ceceocoe
euArgSer GAAACCTT	-1 (1-4322)	Length: Matches: Conservative Mismatches: Indels: Gaps:		42 50-US	.ca , Version	t Encoding Pr t 5840486disk		uTyrPheT : uUACUUGC	OThr	GGUGAACC	CGACAAGC
ProArgLy ::: AATAAAA	22)				n #1.30	rotein of No.		YrGlyLev ::: :UGAAAAUC	CCAAGCUU	erThrTrp :: CGGUGUAI	Ассивес
ProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGlyArg 		4322 84 53 162 111 18		·		Phosphatas		lnAspGlyArgGluValAspTrpGluTyrPheTyrGlyLeuLeuPheThrSer	Val	ArgGluSerArgIleLeuPheSerThTTpAsnLeuAspHisIleIleG ::: ::: ::: BGCAAGAGCCCAAGAUCAUGUUUGUGGUGAACGCGGUGUAUGCCAUGGCCCACGCUUUGC	ACAAACGCAACCACAGGCGCGUCUGCGACAAGCACCUGGCCAUCGACAGCAACUACG
yValAlaGlyArg -GAAGGAGGAGCT						ıse .h Americ		mser 296 ::: GGCU 1326	GluAlaIleLysG ::: ::: GAUGCUAUGAAGA	PHISILEI	CAGCAACU
Arg 24 AGCT 1420					•	ä, Inc.		ğ ,	lug 279 NUCC 1273	TleG 263	246 JACG 1153

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1538 GGTAAGGATGAAGAACAAAGAATATATTTAGGTGTTAATGAAAAAACAAAGA----- 1591
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                                                                                                                                                                                                                                                                        2258 AAGCTACCTCAAGAGACAGCACGAAGTGACAGGCCCATCGAGGTAAAGGAAACA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2138 TCTTCTCTAGCTGATCATGGCATTACTGAGAAAGCAGAAGCTGGTACAGCCTATATAATT 2197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1817 GGCAGCGCTTTAGGAGGGATAACTGGTCAAGTTTGTTCATCAAGAACTGGAAATGTTTTG 1876
                                  2357 CTTTGTCAACGAGATACAGTAGGTGTAATCTATGACAATGATTTTGAAAAGGAATCACGT 2416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2078 AGTTTGAAAGCTACTACAGAAGAATTGTTTACCTGCCAAGAAACAGTGTGCTGTGAACTG 2137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 SerCysLeuSerArgHisSerIle------
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                                                                                                                                                                                                             270 ProThrLeuValGluAlaIleLysGluGlnAspGlyArgGluValAspTrpGluTyr--- 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AspGluGlnAlaProGlnArgGlnArgLeuLeuAlaAspLeuLeuHisAsnValSerGln 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 ValSerAspIleArgArgPheLeuSerAlaPheHisGlu-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 SerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuProGluArgGlySer
                                                                         ------PheTyrGlyLeuLeuPheThrSerGluAsnLeuLysLeuValHis 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTAAAATAAGTGTGGCAGGGATTGGAGCTAGTAACAGAGACCTGGCTACTCTGCTGAGC 1699
                                                                                                                                                         -----GCGTTTGATCCACATGAAGGGAGAAATGATGATTCACATTATACC 2356
                                                                                                                                                                                                                                                                                                                             -----SerThrTrpAsnLeuAspHisIleIleGluLysLysArgThrIleIle 269
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CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 1114
TYPE: DNA
CREMITSM: Mus musculus
US-09-069-023-17
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APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
APPLICANT: Inohara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09069023A Patent No. 6348573
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                                                                                       741 TATGTCCTATGCTGCACAGATGACGGGACAGTTCCTGGTCTA------
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152 LysSerGlyTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluVal 171
                                                                                                                                              135 Arg------AlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSer 151
                                                                                                                                                                                                          681 GGTGTCCTACGACATCCGATGCACCAGGTTCAAGGCCGTGTTAAGGAATCTGCTGAGGTT 740
                                                                                                                                                                                                                                                                 120 AlaAspLeuLeuHisAsnValSerGln------AsnIleAlaAlaGluThr 134
                                                                                                                                                                                                                                                                                                                             636 CCTCGGCTGTCTCAA-----TGT-----CAAAGCCACGATGTACGAGATGTACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 ValSerAspIleArgArg-----PheLeuSerAlaPheHisGluProGlnValGlyLeu
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; OTHER INFORMATION:
US-09-103-840A-2
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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  TTAGCGTTGACCAAT
                                                                                                             TTGTCGTTG-----ATAAGGTTTTGCACCTGGGCCGAGAAAGCGGAGATG------
                                                                                                                                                                  ---TCGGTGAGGATGCGCAGCTGCTCGAGCACA-----TGGTTCAGGTTCGGG 201864
                                                                                                                                                                                                                                                 LeuGlnLysProLysSerValLysLeuArgAla-----LeuArgSerProArgLys 18
                         LeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSerAspIleArgArgPheLeuSerAla 91
                                                                                 TyrPheProSerValProAsp-
                                                                                                                                                                                    PheGlyValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGln 38
                                                                                                                                     LeuProGluArgGlySerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAsp
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                                                      -TTCCCCAGCAGGGCGTCGACCGCGCGCGCGCGCTCGTTGAACGCGGCGATCAGGGTC
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US-09-748-451-2 (1-338) x US-09-103-840A-1 (1-4411529)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37RV
201801 CTGAATCTGCCCAAGATCGTCAGGGTTTCAGCCAAATCCTCCTTGCGGTCGACCAACAGG
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                                           LeuGlnLysProLysSerValLysLeuArgAla-----LeuArgSerProArgLys 18
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Search completed: May 26, 2003, 17:28:03 Job time : 2100 secs

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Command line parameters:

MODEL-frame+_D2n.model -DEV-xlh
-O_/cgn2_1/USPFO_Spool_US09748451/runat_21052003_153830_16347/app_query.fasta_1.519
-OB-Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH-0.1
-LOOPEXT-0 -UNITS-bits -START-1 -END=-1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST-45 -DOKALIGN=200 -THR_SCORE-pct -THR_MAX-100
-THR_MIN=0 -ALIGN=20 -MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-2000000000 -USER-US09748451_@CGN_1_1_57_@runat_21052003_153830_16347
-NCPU-5 -TCPU-3 -NO_MMAP -LARGEDUERY -NCGN_1-1_ST_0FAND-10 -XGAPEXT-0.5
-CONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOB-10 -XGAPEXT-0.5
-FGAPOD-6 -FGAPEXT-7 -YGAPOP=10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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2: //sgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: //sgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

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5: //sgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

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                                    LeuValHisIleValCysHisLysLysThrThrHisLysLeuAsnCysAspProSerArg
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TITLE OF INVENTION: NIKI PROTEIN AND NIKI PROTEIN
FILE REFERENCE: 15966-521 NIK1 protein complexes
CURRENT APPLICATION NUMBER: US/10/242,943
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US/99/167,206
PRIOR EPILICATION NUMBER: US/99/167,206
PRIOR EPILING DATE: 1998-10-06
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TYPE: DNA
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SOFTWARE: PatentIn Ver. 2
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                                                                              GlyLeuGluSerArgPheGlnSerLysSerGlyTyrLeuArgTyr
           TGTGAAGTGGATGCCCTTAAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATG
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                                                               GCCCTGCGCCAGGCAAAGCAGGAGTCCACTGAGTACCGGAGACAGGTGCAGTCCCTCACC
                                                                                                                    GAAGAATGGTACAAATCCAAGTTTGCTGACCTCTCTGAGGCTGCCAACCGGAACAATGAC
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oLysSerValLysLeuArgAlaLe :::	x US-10-161-803-29 (1-1862)	Query Match: 5.73% Indels: 115 DB: 9 Gaps: 16	34.42% Conservative: 20.87% Mismatches:	0.00583 Length: 102.50 Matches:	_	GRGANISH: Homo sapiens		FastSEQ for	PRIOR FILING DATE: 2001-06-01 NUMBER OF SEO ID NOS: 61	CURRENT FILING DATE: 2002-06-03 PRIOR APPLICATION NUMBER: US 60/295.264	PRITCATION NUMBER: US/10/161 803	TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS AND RELATED CONDITIONS	Fairma Chen,	Crip LTip	GENERAL INFORMATION: APPLICANT: Ma. Ylanhong	; Sequence 29, Application US/10161803 ; Publication No. US2003009203841	RESULT 3 US-10-161-803-29	Db 1484 GAATAAAAAGAAATCCATATCTTA 1508	Qy 297 uAsnLeuLysLeuValHisIleVal 305	Db 1424 CATCACGATGACCTTGAATAAAATTGCACACACTCAGTGCAGCAATATATTACCAGCAA 1483	QY 286TrpGluTyrPheTyrGlyLeuLeuPhe-ThrSerG1 297	Db 1370CTGATTAAGACGGTTGAAACTAGAGATGGACAGGTTATCAACGAAACTTCTCAG 1423	uAlaIleLysGluGlnAspGlyArgGlu	Db 1313 AGGGAAACTAATCTGGATTCACTCCCTCTGGTTGATACCCCACTCAAAAAGGACACTT 1369	pHisIleIleGluLysLy	1256GAAGGCGAGGAGAGCAGGATTTCTCTGCCTCTTCCAAACTTTTTCCTCCTGAACCTG 1312	244 TyrSerAsnArgGluSerArgIleLeu	1202 CTCAATGTTAAGATGGCCCTTGACATTGACATTGCCACCTACAGGAAGCTGCTG 1255	Qy 224 PheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHisSerIleAsnPro 243	Db 1196GACCTG 1201	Qy 204 GlySerTyrPheAspArgGlyAlaLysGlyGlySerArgLeuCysThrProGluGlyTrp 223	Db 1142 GATGAGATTCAGAATATGAAGGAGGAAATGGCTCGTCACCTTCGTGAATACCAA 1195	Qy 184 GluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgSerMetGlnTyrAsn 203	Db 1085 GAAGAGAACTTTGCCGTTGAAGCTGCTAACTACCAAGACACTATTGGCCGCCTGCAG 1141	rProSer
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SEQ ID NO 43
; LENGTH: 1864
TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
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TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
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THER INFORMATION: Incyte ID No. US20020156263A1 127987.19
3-974-298-43
    1121 TGTGAAGTGGATGCCCTTAAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATG 1180
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                                                                                                                     144 GlyLeuGluSerArgPheGlnSerLysSerGlyTyrLeuArgTyr----
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                                                                                  GCCCTGCGCCAGGCAAAGCAGGAGTCCACTGAGTACCGGAGACAGGTGCAGTCCCTCACC 1120
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A ArgSerCvsGlnGlnVallenArgI.vsGlvCvsIenArgDheGlnIenDroGlnArgGlv A3	4 LysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGly 23 	1-2 (1-338) x US-10-044-090-793 (1-1892)	Innert Scores: 0.00598	RRENT APPLICATION NUMBER: US/10/044,090 RRENT APPLICATION NUMBER: US/10/044,090 MBER OF SEQ ID NOS: 850 FTWARAE: PERL Program ID NO 793 ENGTH: 1892 YPE: DNA YPE: DNA RGANISM: Homo sapiens RABINES: RABINES: RABINES: RABIONES: RABIONES: RABINES: RABIONES: RABIO	pplication US/10044090 020137081A1 TION: a Bandman TION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE	7 uAsnLeuLysLeuValHisIleVal 305	6	ProThrLeuValGluAlaIleLysGluGlnAspGlyArgGluValAsp 2	6TrpAsnLeuAspHislle	4 TyrSerAsnArgGluSerArgIleLeu	4 PheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHisSerIleAsnPro 243 :::	GACCTG		GluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgSerMetGlnTyrAsn::: ::: ::: GATGAGATTCAGAATATGAAGGAGGAAATGGCTCGTCACCTTCGTGAATACCAA	GAAGAGAACTTTGCCGTTGAAGTGCTAACTACCAAGACACTATTGGCCGCCTGCAG	SerTyrLeuArgGluValSerSe
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US-09-974-298-44
                                                                                        1595 GAATAAAAAAGAAATCCATATCTTA 1619
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                                                                                                                                              297 uAsnLeuLysLeuValHisIleVal 305
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714 AGAAATTGCAGG----
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CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 44
LENGTH: 3405
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ORGANISM: Homo sapiens
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-----SerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGln 183
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Best Local Similarity:
Query Match:
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US-09-981-353-36
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SOFTWARE: PERL PROGRAM
SEQ ID NO 36
LENGTH: 3405
TYPE: DNA
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APPLICANT: Lasek, Amy W.
APPLICANT: Jones, David
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TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0038 US
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HER INFORMATION: Inc
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                                    ArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuProGluArgGly 43
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APPLICANT: HYBRIGENICS

APPLICANT: PLEER, LEGRAIN

TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypepti

TITLE OF INVENTION: mammalian polypeptides

FILE REFERENCE: B4778A
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 561
SOFTWARE: Patentin version 3.1
SEQ ID NO 101
LENGTH: 1218
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Publication No. US20030092028A1
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PRIOR APPLICATION NUMBER: US 60/295,264
PRIOR FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Factor
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  710 GTTGACAATGCGTCTCTGGCACGTCTTGACCTTGAACGCAAAGTGGAATCTTTGCAAGAA 769
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                                                                       GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUD
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOOI103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 3
LENGTH: 69327
                                                                                                                                                                                                                             Sequence 3, Application US/09777921A Patent No. US20020115136A1
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Query Match:
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 AATGTAAAGACCG
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                                                                     AGTGCTTAACTTGGAAAGGAACAATCAGTAC----CAGCCGCTGCAAAATCATGCCAA
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 149
LENGTH: 1749
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APPLICANT: Xu, Jiangchun
APPLICANT: Kalos, Michael D.
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                                                  919 GTTGACAATGCGTCTCTGGCACGTCTTGACCTTGAACGCAAAGTGGAATCTTTGCAAGAA 978
                                                                                                                                             863 --- AGGAGATGCTTCAGAGAGAG-GAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAT 918
                                                                                                                                                                                          44 SerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPheProSerVal 63
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                                                                                              64 ProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSer 83
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                                                                     SEQ ID NO 7
LENGTH: 2673
TYPE: DNA
ORGANIEM: Rattus norvegicus
US-10-060-425-7
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                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10060425
Patent No. US20020164650A1
GENERAL INFORMATION:
APPLICANT: Hiebsch, Ronald
TITLE OF INVENTION: Methods of Assessing Wolframin Protein Activity
FILE.REFERENCE: 00450.US1
                                                                                                                                                                                       CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: 60/266,385
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/060,425
CURRENT FILING DATE: 2002-01-30
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  0.0623
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Qy 292 uLeuPheThrSerGluAsnLeuLysLeuValHis		1953	•	::: 1995 TGTGGAATTGTAGACCTT	 H	2041TCCAGGCCCGTGGCCCACAGGAAGCCATATTGCTGCCA	Qy 236 euSerArgHisSerIleAsnProTyrSerAsnArgGluSerArgIleLeuPheSerT	Db 2077TGCACAGGATCTGGGTCCGGGCCATGTTAGTCTCCT	Qy 216 rgLeuCysThrProGluGlyTrpPheSerCysGlnGlyProPheAspMetAspSerCysL	2133 CACTCGGACATACTTGAAGCGGCCTGTCCACGTGACCCTGTGGCCCTCCAGGTGGC	66 GATGGCCGACTCGGCGC	Qy 181GluAlaGlnGluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgS	Db 2214 ACCGTACAGGCAGCGCATCCAGTCACCCAGGAAGAACGGGAGCATGTT	Qy 162 erArgIleArgSerTyrLeuArgGluValSerSerTyrProSerThrValGlyAla	Db 2248ACGTGTTACCAGAGCTACAGGATGGGTAGGCCTC	Qy 142 heGluGlyLeuGluSerArgPheGlnSerLysSerGlyTyrLeuArgTyrSerCysGluS	Db 2307 GATGTGGCAGGGGTGCTTGGCCAGCTGCTTGAGACGGCAGAGCTCCTCCTCAGCCGTGG	Qy 125 AsnValSerGlnAsnIleAlaAlaGluThrArgAlaGluAspProProTrpP	Db 2349 CATGCCCACTGTGATCTCAAACTTGTAGCGGTCAAACTTCTT		Db 2391 GTCGTCTTCTTCGTGGCCGCGGTT	Qy 85 IleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGlnAlaAlaGln	Db 2451 CAGGTTCAGCAGCACGTCCTTGAACTCGCTGGCTGGCAGGACGATGTCCTTGGTGAT	Qy 76 GlnAlaTrpGln	o IntgluaspryrpneproservalproaspasnalagluLeuvalLeuLeuIntLeuGly 	, ,	2 4 U	2013IGCACCGTGCTACGCCAGTCCTGTTCGAT	25 SerCysGin	2631 AA	36.5	US-09-748-451-2 (1-338) x US-10-060-425-7 (1-2673)	5.39% Indels: 9 Gaps:	Score: 96.50 Matches: 106 Percent Similarity: 35.44% Conservative: 34 Best Local Similarity: 26.84% Mismatches: 125
303	1004	1904	3	1954	273	1996	255	2042	236	2078	2134	199	2167	180	2215	162	2249	142	2308	124	2350	104	2392	84	75 2452	2503	55	2563	4	2616	24			ž.
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	Db 1361AGGGCTTGG	Qy 75 GlyGlnAlaTrp	Db 1325 CTCCCAGAA	Qy 55 LeuThrGluAsp	Db 1283ATCCAG	Qy 35 LeuArgPheGln	Db 1247 TCACCACGCGAP	Qy 15 SerProArgLys	-09-748-451-	Match:		Pred. No.: 0	08-09-995-898A-32	; NAME/KEY: CDS ; LOCATION: (123)(19)	; OTHER INFORMATION: seq ; FEATURE:	; FEATURE: ; OTHER INFORMATION: MBF	; TYPE: DNA ; ORGANISM: Artificial :	; SEQ 1D NO 32 ; LENGTH: 1922	; NUMBER OF SEQ ID NOS:	PRIOR APPLICATION NUMB PRIOR FILING DATE: 200	; PRIOR APPLICATION NUMBE ; PRIOR FILING DATE: 2000	; CURRENT FILING DATE: 2	; TITLE OF INVENTION: CYT; FILE REFERENCE: 00-108	<pre>; APPLICANT: Whitmore, T ; APPLICANT: Grant, Fran</pre>	CANT:	<pre>; Publication No. US200300 ; GENERAL INFORMATION;</pre>	en en		Db 1713 GGCAAAGAGGAA	0у 329	1773	310	Oy 304	Db 1893 CCGAGTCAGGGA

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1893 CCGAGCTCAGGGACTTGACCATTCCCACCAAAAATTGGCCTTGGTCCACGGGAAA 304	β δ	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Alig Pred Scor Perc Best Quer DB:	O O O O O O O O O O O O O O O O O O O	
CCGAGTCAGGGACTTGACCATTCCCACCACCGAAAAGTTGGCCTTGGTCCCACCACCGACAAAGTTGGCCTTGGTCCCACCACCGACAAAGTTGGCCTTGGTCCCACCACCGACAAAGTTGGCCTTGGTCCACCACCGACAAAGTTGGCCTTGGTCCACCACCGACACCGAAAAGTTGGCCTTGGTCCACCACCGACGACACCACTGATTTTGTTGACGTCCACGTCACACCGTTGACTCTTGGTCACACTTGTGTGACACTTTGGTTGACGTCCACGTGACCATGAGTCCATGAGTCCATGAGTCCATGAGTCCATGATTTTTGTTGACACGTCCACGTGACCACCACGTGACCACCACGTGACCACCACGTGACCACCACGTGACCACGTGACCACGATGAGCCAACGCCACCACGATGGGGAAAGCCAACGCACCACGATGGAGCCACGCACCACAGATGGGGAAAACACGAAAGCACACGATGAACCACACGATGAAGCCAACGCACCACAAGTAGCCAACACGATGAAGCCAACGCACCACAAGTAGCCAACACGATGAAGCCAACGCACACAAGTAGCCAACACGATGAAGCCAACGCACCACAAGTAGCCAACACACAC	75 1361	15 1247 35 1283 55 1325	nment Scor l. No.: e: eent Simila Local Sin y Match: 9-748-451-	1893 304 1833 1833 1733 310 310 317 329 329 329 329 329 329 329 329 329 329	
TGACCATTCCCACCGAAAAGTTGGCCTTGGTCACCACCGACCACCACCACCGACCACCGAAAAGTTGGCCTTGGTCACCACCGAAAAGTTGGCCTTGGTCACCACCGACACGAAAGTTGGCCCTTGGTCACCACCGACCG		SerProArgLysi	8) x 95.2455.	CCGAGTCAGGGA CCGAGTCAGGGA AAGCAGGGGCAC TThrHistysLe AAGCAGGGGCAC TThrHistysLe GAACCATCGGGC TThrHistysLe GAACCATCGGGC Application No. US200300 NMATION NO. US200300 NMATION NO. US20030 NMATION NO. US20030 NMATION NO. US20030 NMATION CATTON NUMBER GEARTE COATION NUMBER GEARTION: MBP NMATION: Sequence COBS COATION: MBP NMATION: Sequence COBS COATION COATIO	•
	GlnGlyTyrVals CAACCCCCAGGAT	Phediyvalalad	9-995-898	CTTGACCATTCCC	
	erAspIleArgAr :: GTGACCTATTTTG	ilyargSerCysGl ::: ::: ::: ::: CTTCCCCAGAATG 	Paebt	::: ACCACCGAAAAGT ACCACCGAAAAGT CGTGGTGACCATGA SerArgIleTyri CGCATGAGGGCA CGCATGAGGGCACGG :: ATGGAGGCACGG 	
	gPheLeuSerAl !TGGCCTATCAG <i>I</i>	InGluValLeuA	192 60 24 . 101 60	 TTGGCCTTGGTC IleValCysl ::: XTCTTGGTGAGG; ::: AGGCCAGCCACC 337 1677	
11834 11774 328 1714 1714 1360					
	94 1417	34 1282 54 1324 1360		1834 310 1774 328 1714	

328 uLysArgLysGln 332 ::: ::: 1210 AAAAAAAAAAAA 1222	Qy Db	LeuArgAlaLeuArgSerProArgLysPhe : : :
308 sLysThrThrHisLysLeuAsnCysAspProSerArgIleTyrLysProGlnThrArgLe 328 ::: ::: ::: :::	Qy	5.17% Indels: 10 Gaps:) x US-09-216-393-282 (1-1225)
288 rPheTyrGlyLeuLeuPheThrSerGluAsnLeuLysLeuValHisIleValCysHisLy 308 	Qy Db	Pred. No.: 0.0614 Length: 1225 Score: 92.50 Matches: 81 Percent Similarity: 31.788 Conservative: 35 Best Local Similarity: 22.198 Mismatches: 127
268 eIleProThrLeuValGluAlaIleLysGluGlnAspGlyArgGluValAspTrpGluTy :	Оу	
248 uSerArgIleLeuPheSerThrTrpAsnLeuAspHisIleIleGluLysLysArgThrIl	da Yo	; TYPE: DNA ; CRCANISM: Toxoplasma gondii ; FEATURE: ; NAME/KEY: CDS
238 ArgHisSerIle-AsnProTyrSerAsn	. Oy	NUMBER OF SEQ ID NOS: 364 SOFWARE: PATENTIN VET. 2.0 SEQ ID NO 282 LENGTH: 1225
218 CysThrProGluGlyTrpPheSerCysGlnGlyProPheAspMetAspSerCysLeuSer 237	Qy Db	PLICATION NU LING DATE: 1 PLICATION NU LING DATE: 1
203 AsnGlySerTyrPheAspArgGlyAlaLysGlyGlySerArgLeu 217	Qy	APPLICANT: Milhausen, Michael James TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: TX-1-C2
189 ValleuGlySerMetCysGlnArgLeuArgSerMetGlnTyr	. Qy	
169 ArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGlnGluGluPheLeuArg ::: ::: 799	Qy	Db 1829 CTACACGTTCAGT 1841 RESULT 14
151 SerLysSerGlyTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeu :::	ДУ	Db 1769 AGTCCAGATCACTCTCCAGCCAGCTGCCAGCGAACACCACTGCCTCAGTGCCAGAACCAT 1828 Oy 241 eAsnProTyrSer 245
	Qy Db	::::
111 GinAlaProGinArgCenLeuAlaAspLeuLeuHisAsnValSerGinAsnTle 699	ДУ	Db 1652 TGCCACGTACCAGCTGCCCCCCCTGCATGCCCCCCCTGGATCTGAAGTATGAGGTGGCATT 1711 Oy 206 rPheAspArgGlyAlaLysGlyGlySerArgLeuCysThrProGluGly '222
91 AlaPheHisGluProGlnValGlyLeuIleGlnAlaAlaGlnGlnLeuLeuCysAspGlu 110	Qy	
71 LeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSerAspIleArgArgPheLeuSer 90 :::	Qy	1566
56 ThrGluAspTyrPheProSerValProAspAsnAlaGluLeuVal 70	Qy	QY 150 EXPANSE TUTIL FALL PARKET TO PROTECTIVE THE THE TREE TO PROTECTIVE THE TREE TO PROTE
43 GlySerArgLeuCys	Оу	
30 LeuArgLysGlyCysLeuArgPheGlnLeuProGluArg 42 ::: ::: 430 GTAGCAGGCACCGGATGGCAAGCTAGGTCCACTTCACTGCAGCTTCAACTTCCAACCAA	Qy	Qy 95 ProGlnValGlyLeuIle-GlnAlaAlaGlnGlnLeuLeuCysAspGl 110

CTCTCT -ArgGl 248

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CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION UNUMBER: 08/994,825
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 284
LENGTH: 1225
TYPE: DNA
ORGANISM: TOXOPLASMA GONDALI
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US-09-216-393-284/c
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Patent No. US2001001447A1
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, TITLE OF INVENTION: USES THEREOF FILE REFERENCE: TX-1-C2
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   ValLeuGlySerMetCysGlnArg
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                                                                                                                                                                                                                                                                                                                  GTTTTTTCTGGGAAACGATGGGGGATCTCTTCGTGTGGCGAGACGCTTG
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                                                                                                                 GGCAGGAGCGAGTATACTCGTGGTTGATATACTTTGCGTGGGCGGGTGGCCTCA-----
                                                                                                                                                SerLysSerGlyTyrLeuArg-----TyrSerCysGluSerArgIleArgSerTyrLeu 168
                                                                                                                                                                                  CCTCCTGTTTCAAGGCGGTGAAGTCCG------GAACCGTTGACTTCAAGG-----
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                                                                               ArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGlnGluGluPheLeuArg 188
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US-09-764-891-5984
                                                                                                                                                                                                                                                                                 Score:
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Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Pr
FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Pat
SEQ ID NO 5984
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CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46
                                                                              80 GlyTyrValSerAspIleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeu 99
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                                               ---TATTTGTTGTCTTTTCCTTCTTCTTCTTCT--
                                                                                                                TTCCCTCGCGTCCCC
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               IleGlnAlaAlaGlnGlnLeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeuLeu
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RESULT 17
US-09-764-891-5985/c
; Sequence 5985, Application US/09764891
; Publication No. US20030077808A1
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                                                                                                                                                                                                                                                                       Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 5985 LENGTH: 1282 TYPE: DNA CORGANISM: Homo sapiens US-09-764-891-5985
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                                                          US-09-748-451-2 (1-338) x US-09-764-891-5985 (1-1282)
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Best Local Similarity:
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CURRENT FILING DATE: 2001-01-17
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ITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
'ILE REFERENCE: PC006
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No.:
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60 PheProSerValProAspAsnAlaGluLeuValLeuTeuThrLeuGlyGlnAlaTrpGln ||||||
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APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Bolt, Andrew
APPLICANT: Oblt, Andrew
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREV
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT APPLICATION NUMBER: US/09/834,975
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR APPLICATION NUMBER: 1000-04-14
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US-09-834-975-958/c
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SEQ ID NO 958
LENGTH: 4967
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                 SOFTWARE:
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 Sequence 887, Application US/10091572 Publication No. US20030054373A1 GENERAL INFORMATION:
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                                                                                                                                   ProPheAspMetAspSerCysLeuSerArgHisSerIleAsnPro 243
                                                                                                                                                                                                                                     ACCATTCACAACGCCATGTTCTTCAGCACGTATGACAGAGACAATGACGGCTGGTTAACA 2419
                                                                                                                                                                                                                                                                     Gln---TyrAsnGlySerTyrPhe-----AspArgGlyAlaLysGly-----
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TITLE OF INVENTION: Nucleic Acids, Proteins,
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R APPLICATION NUMBER: 60/
R DATE: 2000-09-2:
                 FILING DATE: 2000-19-25
APPLICATION NUMBER: 60/251,856
FILING DATE: 2000-12-08
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/236,327
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FILING DATE: 2000-09-21
APPLICATION NUMBER: 60/228,924
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APPLICATION NUMBER: 60/180,628
FILING DATE: 2000-02-04
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FILING DATE: 2000-07-26
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FILING DATE: 2000-06-28
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NUMBER: 60/251,868: 2000-12-08
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RR FILING DATE: 2000-09-05
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60/229,513 60/231,413

60/229,287 60/229,345 60/229,343 60/234,997 60/229,344

APPLICATION NUMBER: 60/231,413 FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/229,509

FILING DATE:

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PRIOR APPLICATION UNMBER: 60/249,245
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
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PRIOR REPLICATION NUMBER: 60/249,217
PRIOR REPLICATION NUMBER: 60/249,217
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PR APPLICATION NUMBER: 60/23

PR FILING DATE: 2000-09-08

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REFILING DATE: 2000-09-14
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APPLICATION NUMBER: 60/241, 221
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/246, 475
FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/231, 243
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/231,244
FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/233,064
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APPLICATION NUMBER: 60/249,211
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                                                                                                                                                           94 GluProGlnValGlyLeuIleGlnAlaAlaGlnGlnLeuLeuCysAspGluGlnAlaPro 113
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6264 GAACCACAGGCAGGCCCGGTGACCACAGGGATACTTGTCTTGGTTGTCTCCCCTAGCCAG 6205
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6162 CCCATGTCACAGACAGAAGGGCATTGGGAAGATGGAAAAGCGATTAGAGTCCAGTTAT 610:
                                                                                 6204 CAGCTGGAGAACCCCCTGGCC---
                                                                                                           114 GlnArgGlnArgLeuLeuAlaAspLeuLeuHisAsnValSerGlnAsnIleAlaAlaGlu 133
                                   134 ThrArgAlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSer 153
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                                                                                                                                                                                                                                                                                        Gaps:
                                                                                 ----TGTGGGAACGTAGTCAGGGAA
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OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/240,960
OR FILING DATE: 2000-10-10
OR APPLICATION NUMBER: 60/239,935
OR APPLICATION NUMBER: 60/239,935
OR APPLICATION NUMBER: 60/246,474
OR FILING DATE: 2000-10-02
OR APPLICATION NUMBER: 60/246,474
OR FILING DATE: 2000-11-08
OR APPLICATION NUMBER: 60/246,474
OR FILING DATE: 2000-11-08
OR APPLICATION NUMBER: 60/249,216
OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249,216
OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/226,681
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/225,759
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/225,213
OR APPLICATION NUMBER: 60/225,213
OR APPLICATION NUMBER: 60/225,214
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OR APPLICATION NUMBER: 60/225,214
OR APPLICATION NUMBER: 60/225,214
OR APPLICATION NUMBER: 60/225,314
OR APPLICATION NUMBER: 60/235,836
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/230,438
OR APPLICATION NUMBER: 60/215,135
OR APPLICATION NUMBER: 60/225,266
OR APPLICATION NUMBER: 60/225,266
OR APPLICATION NUMBER: 60/225,014
OR APPLICATION NUMBER: 60/230,438
OR APPLICATION NUMBER: 60/225,266
OR APPLICATION NUMBER: 60/225,014
OR APPLICATION NUMBER: 60/225,014
OR APPLICATION NUMBER: 60/225,014
OR APPLICATION NUMBER: 60/230,438
OR FILING DATE: 2000-09-06
OR APPLICATION NUMBER: 60/225,266

APPLICATION NUMBER: 60/249,218
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,208
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,213
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,213

6163

ביייבא: 60/249,218 2000-11-17 תושחהיי

APPLICATION NUMBER: 60/249,212 FILING DATE: 2000-11-17

DR APPLICATION NUMBER: 60/236,367
DR FILLING DATE: 2000-09-29
DR APPLICATION NUMBER: 60/237,039
DR FILLING DATE: 2000-10-02
DR APPLICATION NUMBER: 60/237,038
DR FILLING DATE: 2000-10-02
DR APPLICATION NUMBER: 60/236,370
DR FILLING DATE: 2000-09-29
DR APPLICATION NUMBER: 60/236,802
DR FILLING DATE: 2000-10-02
DR APPLICATION NUMBER: 60/237,037
DR FILLING DATE: 2000-10-02
DR APPLICATION NUMBER: 60/237,037
DR FILLING DATE: 2000-10-02
DR APPLICATION NUMBER: 60/237,037
DR APPLICATION NUMBER: 60/237,040

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SOFTWARE: PATENTIN Ver. 2
SEQ ID NO 9340
LENGTH: 11598
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-9340
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERAL INFORMATION:
PELICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equence 9340, Application US/09764891 blication No. US20030077808A1
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                                                                            5985 CTTTGT-----ACATTGCAAAGTGGAACCAAGTCATGGGATGAA-----CAG
                                                                                                                                                           6042 --- CCATCTACTGCTGGACCAGCAGGCACGTTCTCTCCAGGCTTCACCCACTGGGGAGC
                                                                                                                                                                                                                                        6102 ACTGCGATTGTTTTCATGGGAACCACTAGGTGTGCCAGCACCAGGCCCCAGAGTGAGCTCC
                                                                                                                                                                                                                                                                                                                      6162 CCCATGTCACAGACAGAAGGGCATTGGGAAGAATGGAAAAGCGATTAGAGTCCAGTTAT 610:
                                                                                                                                                                                                                                                                                                                                                                                                   6204 CAGCTGGAGAACCCCCTGGCC------TGTGGGGAACGTAGTCAGGGAA 6163
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                                                                                                               193 MetCysGlnArgLeuArgSerMetGlnTyrAsnGlySerTyrPheAspArgGlyAlaLys 212
                                                                                                                                                                                    174 TyrProSerThrValGlyAlaGluAlaGlnGlu---GluPheLeuArgValLeuGlySer 192
                                                                                                                                                                                                                                                                             154 GlyTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSerSer 173
                                                                                                                                                                                                                                                                                                                                                            134 ThrargalaGluaspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSer 153
                                                                                                                                                                                                                                                                                                                                                                                                                                        114 GlnArgGlnArgLeuLeuAlaAspLeuLeuHisAsnValSerGlnAsnIleAlaAlaGlu 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 MetCysGlnArgLeuArgSerMetGlnTyrAsnGlySerTyrPheAspArgGlyAlaLys 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 TyrProSerThrValGlyAlaGluAlaGlnGlu---GluPheLeuArgValLeuGlySer 192
                                     213 GlyGlySerArgLeuCysThrProGluGlyTrp 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 GlyGlySerArgLeuCysThrProGluGlyTrp 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 GlyTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 GluProGlnValGlyLeuIleGlnAlaAlaGlnGlnLeuLeuCysAspGluGlnAlaPro 113
GGTGGCCCAGAGTTAGCATTCCCAGAGGCCTGG
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CTTTGT------CAGTTGCAAAGTGGAACCAAGTCATGGGATGAA-----CAG
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Search completed: May 26, 2003, 16:58:10 Job time: 230 secs

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Title:
Perfect score:
Sequence:
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MODEL=frame+_p2n.model -DEV=xlh

-Q-\cgn2_1/\cgn2_prol_\US09974845\/\runat_21052003_153830_16291\app_query.fasta_1.519

-Q-\cgn2_1/\usuprol_spool\\usuprol_spool\\usoprol_1\usuprol_spool\\usuprol_1\usuprol_spool\\usuprol_1\usuprol_spool\\usuprol_1\usuprol_spool\\usuprol_1\usuprol_spool\\usuprol_1\usuprol_spool\\usuprol_1\usuprol_spool\\usuprol_1\usuprol_1\usuprol_spool\\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_1\usuprol_
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Ygapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1789
1 MLQKPKSVKLRALRSPRKFG.....SRIYKPQTRLKRKQPVRKRQ 338
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	C 44	43	c 42	41	c 40	39	38	37	w	c .35	34	33	32	31	c 30	29	28	c 27	26	25	24	23	22	21	c 20	19	18	17	16	c 15	14	1 1	12	110	0		c 7	١٥١	51	4	w	2	_	NO.	Kesuic	1
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ALIGNMENTS

AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BQ715165	RESULT 1
NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1014)	Mus musculus	house mouse.	EST.	BQ715165.1 GI:21854064	BQ715165	5', mRNA sequence.	s musculus	BQ715165 . 1014 bp mRNA linear EST 16-JJIL-2002		

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Plate: LLAM13731 row: j column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan,
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                                                             HisileIleGluLysLysArgThrIleIleProThrLeuValGluAlaIleLysGluGln 279
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GATGGGAGGGAGGTGAACTGGGAGTACTTCTACAGCCTGCTCTTCACTGCCGAGAACCTG 534
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                                                 CCAGAAGGATGGTTCTCCTGCCAGGGCCCCTTTGACCTGGAGAGCTGTCTTTCCAAGCAC
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             21 ValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuPro 40
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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Clone distribution: MGC clone distribution information can
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall Site_2: NotI; Cloned unidirectionally. Primer: Oligo dy Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Grow and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:5325440"
/clone_11b="NCI_CGAP_Mam4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                           Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata;
Eutheria; Rodentia;
Mammaila; Eutheria; Rodentia;
1 (bases 1 to 834)
                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM10830 row: a column: 05
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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602796717F1 NCI_CGAP_Mam4 Mus
                                                                                                                                                                         Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
                                                                                                                                                                                                                                                                                                                                                        house mouse.
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                                                                                                                                                                                             tact: Robert Strausberg, Ph.D.
il: cgapbs-r@mail.nih.gov
                    quality sequence stop:
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                    788.
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                                                          201 GlnTyrAsnGlySerTyrPheAspArgGlyAla---LysGlyGlySerArgLeuCysThr 219
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ProGlu-GlyTrpPheSerCysGlnGlyProPhe-AspMetAspSerCysLeuSerArgH
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a. 236 c 240 g 172 t
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/db_xref="taxon:10090"
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/dev_stage="5 months"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Mam4"
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                                                                                                                                                                                             Query Match:
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High quality sequence stop: 685.
Location/Qualifiers
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Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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Plate: LLAM11404 row: b column:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                          ValAlaGlyArgSerCysGlnGluValLeuArg-LysGlyCysLeuArgPheGlnLeuPr 40
       GTGGCTGGCCGGAGCTGCCAGGAGGTGCTGCTGCAAGGGCTGTCTCCGCTTCCAGCTCCC
                                                                          isSerIleAsnProTyrSerAsnArg-GluSerArgIleLeuPheSerThrTrpAsnLeu 258
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                                                                                                                                                                                                                                                                                                                                                                 /lab_host="univo"
/note="Organ: pooled colon, kidney, stomacn; recover.
pcMv-spORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:5162791"
/clone_lib="NIH_MGC_116"
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/db_xref="taxon:9606"
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Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                                                            http://image.llnl.gov
Plate: LLAM11513 row: p column:
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gIleArgSerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACAACGTCAGCCAGAACATCGCGGCCGAGACCCCGGGCTGAGGACCCGGCGTGGTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGACATCAGGCGCTTCCTCAGTGCATTTCACGAGCCACAGGTGGGGCTCATCCAGGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTG-ATGTGTCTTCTGCTGGACCGGCACCTTTTGTTTGTCCCATTGGTGGCAGATGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 830)
/note-*Organ: pooled lung and spleen; Vector: pCMV-SPORT6 Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size
                                                                                                              /clone_lib="NIH_MGC_122"
/lab_host="DH10B"
                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5204996"
                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
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141 TrpPheGluGlyLeuGlu-SerArgPheGlnSerLysSerGlyTyrLeuArgTyrSerCy
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684 GACTC-CTGCACAACGTCAGCCAGAACATCGCGTGGGAGACCCGGGGTGAGGACCCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                624 CAGGCCNGCCAGCAGCTGCTGTGTGATGAGCAGGCCCCACAGAGGCAGAGGCTGCTGCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         564 TATGTGAGCGACATCAGGCGCTTCCTCAGTGCATTTCACGAGCCACAGGTGGGGCTCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 GluArgGlySerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPhe
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 855)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: Capabs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnAlaAlaGlnGlnLeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeuLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuPro
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249 c 280 g 155 t 1 others
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DB:
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Best Local Similarity:
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                                                                                           541 GAGAGTCGGATCCGGGGTTACCTAAGAGAGGTGAGCGCTTACACCTCTATGGTGGATGAA
                                                                                                                     161 GluSerArgIleArgSerTyrLeuArgGluValSerSerTyrProSerThrValGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 TATGTGAGTGACATCACACGTTTCCTCAGTGTGTTTAATGAGCCACATGCCGGCGTCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://insge.llnl.gov
plate: LLAM9270 row: j column: 04
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Location/Qualifiers
                                                                                                                                                                                                           TrpPheGluGlyLeuGluSerArgPheGlnSerLysSerGlyTyrLeuArgTyrSerCys 160
                                                                                                                                                                                                                                                                         GATCTTCTGCATCACGTGAGCCAGAATATTACTGCAGAGACCCGGGAGCAGGACCCATCC
                                                                                                                                                                                                                                                                                                                AspLeuLeuH1sAsnValSerGlnAsnIleAlaAlaGluThrArgAlaGluAspProPro
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       GCAGGTCGAGAAGAGTACCTGNCGAGTCCTTGGGTCCATGTGCAG-AAGCTCAAATCGGT
                                                                                                                                                                                   TGGTTTGAAGGTTG-GAGTCGAGATTCAGGAATAAGTCGGGCTATCTGAGATACAGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. primer: Oligo (Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" a 215 c 285 g 174 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:419943"
/clone_lib="NCI_CGAP_Lu29"
/tlssue_type="spontaneous tumor, metastatic stem cell origin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
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/strain="CZECH II"
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Mus musculus house mouse

REFERENCE

TITLE

COMMENT

RESULT 6 BF165515

DEFINITION

mRNA sequence. BF165515

BF165515.1 GI:11045867

BF165515 855 | 601777413F1 NCI_CGAP_Lu29 Mus

bp mRNA : s musculus cDNA

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Percent Similarity: Best Local Similarity:

6.81e-82 774.00 94.678 94.678 43.268

Length:
Matches:
Conservative:
Mismatches:
Indels:

Gaps:

Query Match:

-748-451-2 (1-338) x BI770511 (1-830)

Alignment Scores:

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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Tissue Procurement: Life Technologies,
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National Institutes of Health, N
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1 (bases 1 to 775)
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                          rValSerAspIleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGl 101
                                                                       SerValProAspAsnAlaGluLeuValLeuThrLeuGlyGlnAlaTrp-GlnGlyTy 81
TGTGAGTGACAT - CGGTGCTTCCTCAGTGCTTTTCGCCAGCCGCACGCGTGGCTCATCCA
                                                        ProGluGlyTrpPheSerCysGlnGlyProPheAspMetAspSerCys
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                                                                                                                                                                                                                                                                         (Invitrogen). Research Genetics
this is a NIH_MGC Library."
a 233 c 239 g 152 t
                                                                                                                                                                                                                                                                                                                  full-length clones and
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/clone_11b="NIH_MGC_121"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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th clones and was constructed by C. Gruber
en). Research Genetics tracking code 017..Note:
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181 GluAlaGluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgSerMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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http://image.llnl.gov
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AGENCOURT_7786920 NIH_MGC_92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Institutes of Health,
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/tissue_type="embryonal carcinoma, cell line"
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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies
                                                                                                                                                                                  /organism="Homo sapiens"
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RESULT 9 BQ055307/c LOCUS DEFINITION AGENCOURT_6797380 NIH_MGC_99 Homo sapiens cDNA clone TMAGE:5807463 **ACCESSION BQ055307.1 GI:19814647 **KEYWORDS SOURCE human.** CORGANISM Homo sapiens **CORGANISM Homo sapiens **EVENT EST.** **DURBAL Library Preparation: Rubin Laboratory **REFERENCE NIH MGC http://mgc.ncl.nih.gov/ **COMMENT Contact: Robert Strausberg, Ph.D. **Email: cgapbs-remail.nih.gov/ **Tissue Procurement: Lou Staudt **CDNA Library Preparation: Rubin Laboratory **Tissue Procurement: Lou Staudt **CDNA Library Preparation: Rubin Laboratory **Tissue Procurement: Lou Staudt **CDNA Library Preparation: Rubin Laboratory **Tissue Procurement: Lou Staudt **CDNA Library Preparation: Rubin Laboratory **Tissue Procurement: Lou Staudt **COMMENT COMMENT C	Oy 157 9Tyr-SercysGluSerArgIleArgSer-TyrLeuArg-cluValSerSerTyrPr 175 1111	Oy 120 AlaAspLeuLeuHisAsnValSerGinAsnIeAla AlaGluThrArgAlaGluAsppr 139		OS-09-748-451-2 (1-338) x H0431184 (1-908) OY MetLeuGlilysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGly 20 OY IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OUNT 158 a 271 c 3 ent Scores: 7.15e-75 NO.: 716.00 t Similarity: 87.318 ocal Similarity: 85.798 Match: 40.028
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149 edlnserLysserGlyTyrL	110 uglnala-ProGlnargGln	76 GINALSTIPGINGLYTYVVa ::: ::: 921 AGGGCTTGGCAGGGCTTATT 91 AlaPheHisGluProGlnVa TTCGCCAGCCGGCAGGC	Library." GIN 248 a 344 c GIN 346 c 347 c 348 c 358 c 368 c 378 c 388	/clone="lkAGE /clone="lkaGE /clone="lb="NI /lash host="DH="NI /note="Organ: ECORL; CDNA mi into ECORL/XhA into	cDNA Library Arrayed DNA Sequencing by: Ag Clone distribution: M found through the I.M. found through the I.M. plate: LICM2049 row: Plate: LICM2049 row: High quality sequence

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/organism="Homo sapiens"
/odb.xref="taxon:9606"
/obcone="Interest | Colone="Interest |
/clone=Interest | Colone=Interest |
/clone=Interest rary."
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11n1.gov
049 row: o column: 16
sequence stop: 595.
278 g
         201 t
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x BQ055307 (1-1071)

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

AlaPheHisGluProGlnValGlyLeuIleGlnAla-AlaGlnGlnLeuLeuCysAspGl TTCGCCAGCCGGCAGGCGGGGTTCATCCAAGCCCGCCGGCAGTTACTGTGTGATGA
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DEFINITION
ACCESSION
VERSION
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Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html
Location/Qualifiers
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Buerstedde, J.M.
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Gallus gallus
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AJ451681
AJ451681.1 GI:20261777
EST.
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Unpublished (2002)
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                                                                                                                                                                                                            CTGTGCCTCTACGAGGACGGACGGAGCTGAGCGAGGCGTTCTTCCGCACGCTGCCGCCG
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|CAGGCTCCTCTGGACCTGGAAC
              ValSerGlnAsnIleAlaAlaGluThrArgAlaGluAspProProTrpPheGluGlyLeu
                                                                                                                                                     CAGACGGAGCTGCTGCTGCGGCCCGGGGAGAGCTGGCCGGGC---
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                                                                     LeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeuLeuAlaAspLeuLeuHisAsn
                                                                                                                           ArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGlnAlaAlaGlnGln 105
                                                                                                                                                                               AsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSerAspIle
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/db_xref-"taxon:9031"
/clone-"29j11r1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
/note="CB inbred strain"
/172 c 219 g 132 t
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Neognathae; Galliformes; Phasianidae;
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                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10726 row: k column: 01
                                                                                                                                                                           Email: cgapbs-r@mail.nlh.gov.
Tissue Procurement: Miklos Pakkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI),
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Library Arrayed by: The I.M.A.G.E.
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 716)
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EST.
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602688206F1 NIH_MGC_95
                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                e: LLAM10726 row: k column: quality sequence start: 10 quality sequence stop: 573. Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4820856"
/clone_lib="NIH_MGC_95"
                                                                                                                                                                                                                                                                                                                                                                                          GI:13979919
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IMAGE:4820856 5',
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BASE COUNT ORIGIN

Query Match:

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US-09-748-451-2 (1-338) x BG705510 (1-716)
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BB619078 RTKEN full-length enriched, 8 days
cDNA clone 5730477D02 5', mrNA sequence.
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/lab_host="DH10B"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurrognathi; Muridae; Mus.

1 (bases 1 to 614)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,

Hiramoto,K., Hori,F., Ishil,Y., Ito,M., Kawai,J., Konno,H., Kouda,

M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,

Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki

Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki

Do, Shibatta,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,

Tagami,M., Tagawa,A., Takhashi,F., Takeda,Y., Tanaka,T., Toya,T.,

Muramatsu,M. and Haysahizaki,Y.

RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

Onpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It
Carninci,p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraris for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujlwake,S., Incue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuu
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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Caboratory for Genome Exploration Research Group, RIKEN Genomic
Eaboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9216
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BB619078.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computational Analysis of Full-Length Mouse cDNAs Compared with Numan Genome Sequences Mamm. Genome. 12, 673-677 (2001)
prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 100.0 Second strand cDNA was prepared with the
                                                                                                                     contributed to prepare mouse tissues. 1st strand cDNA was grimed with a primer [5' GAGAGAGAGAGCAGTCTTTTTTTTTTTTTTTTTTVN 3'], cDNA was contributed to prepare mouse tissues.
                                                                                                                                                                                                                                   /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="5730477DD2"
/clone="15730477DD2"
/clone=158-RIKEN full-length enriched, 8 days embryo"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="8 days embryo"
/lab_host="DH10B"
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Shibata, K., Itoh

T., Matsuura

230-0045, Japan

В δõ В å 밁 γQ ₽

QΥ 밁 Š В Qy B

вв619078 RESULT 12 DEFINITION

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SOURCE
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8138
                                                                                 AUTHORS
TITLE
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source
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                 Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
                                                 Contact: Buerstedde JM
Cellular Immunology
                                                                                                              Archosauria; Aves; Neognathae; Phasianinae; Gallus.
                                                                                                                                            Gallus gallus
                                                                     Unpublished (2002)
                                                                               Gallus gallus bursal lymphocyte
                                                                                           Buerstedde, J.M.
                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                       chicken
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585.00
84.52%
72.26%
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                                                                                                                                                                                              Gallus gallus
                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae;
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TINTTNTTGTCAAGGGCCCCTTTTTGAC
                                                                                                                                        CTACTTTGACAGGACAGGAGGAGGCGCGCGATGCGCCTNTTCACAAAGGGAGGGAATGG
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/clone_lib="riken1"
/clone_lib="riken1"
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/dev_stage="2-3 weeks old"
/note="CB inbred strain"
/note="CB inbred strain"
/note="CB 275 g 129 t
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/db_xref="taxon:9031"
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             637 bp mRNA (synonym: hlcc3) H
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                                                                                                                                                                                                                                                                                                                                                               612 TACAGTAACAGGGAGAGCAGGATC 635
                                                                                                                                                                                           204 GlySerTyrPheAspArgGlyAlaLysGlyGlySerArgLeuCysThrProGluGlyTrp
                                                                                                                                                                                                                                                                                                                       164 IleArgSerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGln
                                                                                                                                                                                                                                                                 184 GluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgSerMetGlnTyrAsn
                                                                             244 TyrSerAsnArgGluSerArgIle 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dKfz- heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
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AL602837.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No sl sequence available.
This clone (DKFZp68601116) is available at the R2PD in Phlase contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wambutt
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EST (Wanbutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
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                                                                                                            TTCTCCTGCCAGGGTCCCTTTGACATGGACAGCTGCTTATCAAGACACTCCATCAACCCC
                                                                                                                                        PheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHisSerIleAsnPro
                                                                                                                                                                         GGCAGCTACTTCGACAGAGGAGCCAAGGGCGGCAGCCGCCTCTGCACACCGGAAGGCTGG
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cDNA-collection"
172 c 190 g 135 t
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/db_xref="taxon:9606"
/clone="DKFZp68601116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone-"DKFZp68601116"
/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
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US-09-748-451-2 (1-338) x AQ422321 (1-526)
                                                                           347 -----GTCCTCGACGATGCCGAGCTGGTGCTCACCTCACGCCAGGCCTGGCAGGGC
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                                                                                                                                                                                                                                                                                                                                                                 498 GTGCTCCAGAAGCACAAGACTGTGAAGCTGCGGGCCCTGTGCAGCCCGAGGAAGTTTGGC
                                                                                                      61 ProSerValProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGly 80
81 TyrValSerAspIleArgArgAheLeuSerAlaPheHisGluProGlnValGlyLeuIle 100
                                                                                                                                                                                                                      41 GluArgGlySerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPhe 60
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Clones are derived from the human BAC library RPCI-11. For BAC Clones are derived from the human BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (lnfo@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 526)
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RPCI-11-186H3.TV RPCI-11
DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
176 c 147. g 102 t
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/Clone="RPCI-11-186H3"
/Clone_11b="RPCI-11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:7571210"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3124 row: D column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H3124D06-5 NIA Mouse 15K cDNA
H3124D06 5', mRNA sequence.
BG086312
BG086312.1 GI:12568876
EST.
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Seq primer: -21M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other_ESTs: H3124D06-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K.,
,T.S., Carter,M.G. and Ko,M.S.H.
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1 (bases 1 to 515)
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Mammalia; Eutheria; Rodentia;
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        aAspLeuLeuHisAsnValSerGlnAsnIleAlaAlaGluThrArgAlaGluAspProPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ional Institute on Aging/National Institutes of Health Cassell Drive, Suite 4000, Baltimore, MD 21224-6820,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 515
                                                     /note-"Vector: psport; Site_1: Sali; Site_2: Noti; This clone is among a rearrayed set of 15,247 clones from 11 embryo coMA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb All
            source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide
                                                                                                                                                                                                                                      /clone="H3124D06"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:H3124D06-5"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                      /lab_host="DH10B"
profiling
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of mid-gestation
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                              BI789500 537 bp mRNA linear LEST 12-MAR-2002 ic95e08.yl Melton Normalized Mixed Mouse Pancreas 1 NI-MMSI MUS musculus cDNA clone IMAGE:5661422 5' similar to TR:054788 054788
CAD PROTEIN. ;, mRNA sequence. BI789500
                                                                                                                                                                        TrpPheGlu 143
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Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse develolpment, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex
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72.73%
30.80%
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Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hilller,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.
Schmitt, A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Carder,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams

Bennett, J., Carca Bennett, J., Carca Bennett, J., Williams, T

Permutt, A.,

Lee,C

, Kaestner, K.,

Mammalia; Eutheria; 1 1 (bases 1 to 537) Melton,D., Brown,J.,

Eukaryota; Metazoa; Mus musculus

Chordata; Rođentia; Kenty, G.,

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

BI789500.1 house mouse

GI:15817225

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Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
MGI:1947748 This sequence now available from the IMAGE consortium,
for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 436.
Location/Qualifiers
                                                                                                                                                                                                                                                                 Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept_of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MA 02138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adult, mixeu
/lab_host="NHIOB"
/lab_host="NHIOB"
/note="Vector: pspORT1; Site_1: Not i; Site_2: Sal I; Five
/note="Vector: pspORT1; Site_1: Not i; Site_2: Sal I; Five
/note="Vector: pspORT1; Site_1: Spancreatic bud, E16.5
/note=seenting E10.5/12.5 pancreatic and adult
ilbraries representing E10.5/12.5 pancreatic and adult
islets of Langerhans were seperately constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
was made by oligo-df priming and size-selected by column
fractionation. Libraries were amplified once on solid
support and plasmid DNA from each library was prepared
and mixed in equal amounts. The mixed library DNA was
normalized by method #4 from Bonaldo, Lennon, and Soares
1996 Genome Research 6:791-806; 0.5 microgram
single-stranded mixed library plasmid DNA was mixed with
5 micrograms PCR product representing mixed library
inserts and hybridized to an Ecot of 6. Single-stranded
(unhybridized) plasmids were isolated by hydroxyapatite
chromatography and used to make this library."
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/clone="IMAGE:5661422"
/clone_lib="Melton Normalized Mixed Mouse Pancreas 1
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/strain="ICR"
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Unpublished (2001)
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Normalization and subtraction of cap-trapper-selected coNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiawke, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9212
Fax: 81-45-503-9216
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 643)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,F.
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BB628807 RIKEN full-length enriched, 16
musculus cDNA clone 9630035119 5', mRNA
                                                                                                                                                                                                                                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                      Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fikuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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Human Genome Sequences.

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                                 ValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuPro
-ProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSerGly
                                                                                CAGGCTGCACGGCAACTGCTGTCAGATGAGCCAGGCCCCACTGAGGCAAAAGCTGCTGGCC
                                                                                                                               TATGTGAGTGACATCACACGTTTCCTCAGTGTGTTTAATGAGCCACATGCCGGCGTCATC
                                                                                                                                           TyrValSerAspIleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIle
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/lab_host="DH10B"
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/clone="9630035119"
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AUTHORS
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                                                                                                     21 ValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuPro
                                                                                                                                                                                Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.I. Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heatcon, M.F., Laegreid, W.M., Rohrer, G.A., Chitko-McKown, C. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACKWARD: GTTTTCCCAGTCACGACG Plate: 59 row: D column: 7 Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
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PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4356
Fax: 402 762 4390
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ATCCCTGGTTCCCGCCTGTGTCTCTATGAGGATGGCACGGAATTGACTGGAGATTACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Bos taurus"
/db_xref-"taxon:9913"
/clone_lib-"MARC 2BOV"
/tissue_type-"pooled"
/lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Library made from pooled tissue from testis, thymn semitendonosus muscle, longissimus muscle, pancrea adrenal, and endometrium."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryzias latipes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.

1 (bases 1 to 688)
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BJ026619
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Location/Qualifiers
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Medaka EST project in Takeda's lab
Unpublished [2001]
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/clone_lib="MF01SSA cDNA"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25
a 172 c 178 g 205 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryzias latipes"
/strain="Hd-rR"
                                                                                                                                                                          1.21e-47
487.50
71.60%
55.56%
27.25%
                                                                                                                                                                                          Conservative: Mismatches: Indels:
                                                                                                                                                                        Gaps:
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Matches:
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90
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                                                                                  320 ArgileTyrLysProGlnThrArg------LeuLysArgLysGlnProValArgLys 336
                                                                                                                       188 AGGCGA 183
                            337 ArgGln 338
                                                             248 ATGGCGGTGAGGGCCTCCAGCCACGCAGGGGGAGTGAAGAAGAAGGTCCAGGTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                     280 AspGlyArgGluValAspTrpGluTyrPheTyrGlyLeuLeuPheThrSerGluAsnLeu 299
                                                                                                                                                                                                                                                       428 CACAGGATTGAGAAGAAGAGGACCGTCATTCCCACGCTGCTGGAGCTCCTAGAGACTCAC 369
                                                                                                                                                                                                                                                                                         260 HisIleIleGluLysLysArgThrIleIleProThrLeuValGluAlaIleLysGluGln 279
                                                                                                                                                                                                                                                                                                                         488 TCCATCAACCCCTACAGCAGCAGGAGGAGCAGGATCATCTTCAGCACCTGGAACCTGGAC
                                                                                                                                                                                                                                                                                                                                                     240 SerIleAsnProTyrSerAsnArgGluSerArgIleLeuPheSerThrTrpAsnLeuAsp 259
                                                                                                                                                                                                                                                                                                                                                                                      548 CAGCAGGGATGGTTCACCTGCCAGGGACCGTTTGACCAGAGGACGTGCCAGCAGCTCCAC 489
                                                                                                                                                                                         309
                                                                                                                                                                                                                                                                                                                         429
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Search completed: May 26, 2003, 16:52:57 Job time: 1715 secs

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